

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 23:55:46 ; Search time 2057 Seconds
(without alignment)
4393.830 Million cell updates/sec

Title: US-10-691-412-1
Perfect score: 159
Sequence: 1 atggagaaagtcacacac.....tcacgtgatcttctga 159

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	323	8	HUMPLAM
2	159	100.0	480	6	BD030469
3	159	100.0	480	6	AX894936
4	159	100.0	980	8	HSPLBG2
5	159	100.0	1635	6	CQ118671
6	159	100.0	1635	6	AX329653
7	159	100.0	1635	8	HUMPHLAM
8	159	100.0	1691	8	BC005269
9	159	100.0	1712	6	CS115190
10	159	100.0	60797	14	AL355356
11	159	100.0	66092	14	AL136974
12	159	100.0	150290	8	HS509L4
13	144.6	90.9	159	6	BD247911
14	144.6	90.9	159	6	AR302007
15	144.6	90.9	159	6	AX040491
16	144.6	90.9	858	4	RASPFLAM2
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18	143	89.9	159	6	AR302003

19	143	89.9	159	6	AX040487
20	143	89.9	737	4	SSPLB
21	143	89.9	2841	4	OCPLAM
22	139.8	87.9	314	4	AY514751
23	139.8	87.9	669	4	AY576871S2
24	139.8	87.9	832	4	DOGPHL
25	139.8	87.9	832	4	DOGPLBA
26	139.8	87.9	2614	4	CFPHLX
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28	128.6	80.9	648	9	BC061097
29	128.6	80.9	940	9	S46792
30	128.6	80.9	167574	9	AC153524
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37	125.4	78.9	231910	14	AC128365
38	123.8	77.9	701	9	RNPHLAM
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43	74.2	46.7	133901	5	BS537355
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45	41.4	26.0	179556	14	AC013809
46	36.8	23.1	134286	8	AC025771
47	36.8	23.1	170272	8	AC024589
48	36.4	22.9	116103	8	AL590653
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50	35.4	22.3	141913	8	AL512452
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68	34.8	21.9	151900	8	AC096644
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73	34.8	21.9	178371	5	BX005174
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76	34.8	21.9	251443	14	AC096251
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85	34.4	21.6	246901	14	AC108350
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87	34.4	21.6	263578	14	AC015657
88	34.2	21.5	805	10	BV054436
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AY514751 Canis fam
AY576872 Canis fam
M16012 Canine card
M35393 Dog cardioc
Y00399 Dog phospho
BC061097 Mus sapi
S46792 phospholamb
AC153524 Mus muscu
CQ447405 Sequence
AC100317 Mus muscu
S95853 phospholamb
S95849 Rattus sp.
L03382 Rat phospho
AC097906 Rattus no
AC128365 Rattus no
X1088 R.norvegicu
MS9039 Chicken car
MS9038 Chicken pho
AR121629 Sequence
CR926459 Zebrafish
BS537355 Zebrafish
BS276081 Zebrafish
AC013809 Homo sapi
AC025771 Homo sapi
AC024589 Homo sapi
AL590653 Human DNA
AL158428 Ornithorh
AL512452 Human DNA
AL109913 Human DNA
AC164940 Atelerix
AB042236 Homo sapi
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AP002531 Homo sapi
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AL18393 Rattus no
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AC110891 Mus muscu
BX005174 Zebrafish
CR391977 Zebrafish
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AF078533 Homo sapi
AC095653 Rattus no
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AC114844 Rattus no
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AC111814 Rattus no
AC108350 Rattus no
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Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCAATTGAATG 60
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Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 315

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Db 316 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 354

RESULT 4
HSPLEB2
LOCUS Homo sapiens phospholamban gene, exon 2 and complete cds.
DEFINITION AF177764
ACCESSION AF177764.1 GI:5916236
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS McTiernan, C.F., Frye, C.S., Lemster, B.H., Kinder, E.A., Ogletree-Hughes, M.L., Moravec, C.S. and Feldman, A.M.
TITLE The human phospholamban gene: structure and expression
J. Mol. Cell. Cardiol. 31 (3), 679-692 (1999)
PUBLISHED 10198197
REFERENCE 2 (bases 1 to 980)
AUTHORS McTiernan, C.F., Frye, C.S., Lemster, B.H., Kinder, E.A., Ogletree-Hughes, M.L., Moravec, C.S. and Feldman, A.M.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1999) Cardiovascular Institute, University of Pittsburgh, 200 Lothrop St., Pittsburgh, PA 15213, USA
JOURNAL Location/Qualifiers
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Db 192 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 251

Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 159
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RESULT 5
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LOCUS Homo sapiens (human)
DEFINITION Sequence 4605 from Patent WO02068579.
ACCESSION Qy18671
VERSION Qy18671.1 GI:42279528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 4605 06-SEP-2002;
PE Corporation (NY) (US)
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Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 340

RESULT 6
AX329653
LOCUS Homo sapiens (human)
DEFINITION Sequence 162 from Patent WO0194629.
ACCESSION AX329653
VERSION AX329653.1 GI:18102631
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 162 13-DEC-2001;
Avalon Pharmaceuticals (US)
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340

RESULT 7

HUMPHLAM 1635 bp mRNA linear PRI 07-JAN-1995
 LOCUS Human phospholamban mRNA, complete cds.
 DEFINITION M63603
 ACCESSION M63603.1 GI:189942
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1635)
 FUJII,J., ZARAIN-HERZBERG,A., WILLARD,H.F., TADA,M. and MACLENNAN,D.H.
 TITLE Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6
 J. Biol. Chem. 266 (18), 11669-11675 (1991)

JOURNAL PUBMED 1828805
 COMMENT Original source text: Homo sapiens cDNA to mRNA.
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Qy	61	CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
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RESULT 9		
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LOCUS	CS115190	1712 bp DNA linear PAT 08-JUL-2005
DEFINITION	Sequence 1 from Patent EP1548131.	
ACCESSION	CS115190	
VERSION	CS115190.1	GI:70663800
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mizrahi, J. and Ostenson, C.G.	
TITLE	Novel targets for obesity from skeletal muscle	
JOURNAL	Patent: EP 1548131-A 1 29-JUN-2005;	
	F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)	
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Qy	61	CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
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	* 42154	44594: contig of 2441 bp in length
	* 44595	44694: gap of 100 bp
	* 44695	48031: contig of 3337 bp in length
	* 48032	48131: gap of 100 bp
	* 48132	50319: contig of 2188 bp in length
	* 50320	50419: gap of 100 bp
	* 50420	53189: contig of 2770 bp in length
	* 53190	53289: gap of 100 bp
	* 53290	55344: contig of 2055 bp in length
	* 55345	55444: gap of 100 bp
	* 55445	57739: contig of 2295 bp in length
	* 57740	57839: gap of 100 bp
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Qy      121  TGCTCTTGTGTGATCTGTATCATCTCGTGATGCTCTCTCTGA 159
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RESULT 11
AL136974
LOCUS      Homo sapiens chromosome 6 clone RP3-436C16, 2 unordered pieces.
DEFINITION
ACCESSION  AL136974
VERSION    AL136974.4 GI-9930800
KEYWORDS  HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
1
REFERENCE  1
AUTHORS   Williams,S.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
           CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT   requests: clonerquest@sanger.ac.uk
           On Aug 27, 2000 this sequence version replaced gi:9863476.
           ----- Genome Center
           Center: Sanger Centre
           Center code: SC
           Web site: http://www.sanger.ac.uk
           Contact: humquery@sanger.ac.uk
           Project Information
           -----
           Center project name: dJ436C16
           ----- Summary Statistics
           Assembly program: XGAP4; version 4.5
           Sequencing vector: plasmid; L08752; 100% of reads
           Chemistry: Dye-terminator Big Dye; 100% of reads
           Consensus quality: 65294 bases at least Q40
           Consensus quality: 65764 bases at least Q30
           Consensus quality: 65936 bases at least Q20
           Insert size: 65992; sum-of-contigs
           Insert size: 77256; 1.8% error; agarose-fp
           Quality coverage: 8.00x in Q20 bases; sum-of-contigs Quality
           coverage: 7.55x in Q20 bases; agarose-fp
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           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 2 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           * 1 63797: contig of 63797 bp in length
           * 63798 63897: gap of 100 bp
           * 63898 66092: contig of 2195 bp in length.
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FEATURES
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misc_feature

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Query Match 100.0%; Score 159; DB 14; Length 66092;
 Best Local Similarity 100.0%; Pred. No. 4e-32;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CCTCAACAGACAGCTCAAAAGCTACAGATCTATTATCAATTTCTCTCTCACTTTAATA 120
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QY 121 TGCTCTTGTGATCTGTATCATCTGATGATCTTCTCTGA 159
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RESULT 12

LOCUS

HS509L4 150290 bp DNA linear PRI 18-MAY-2005
 Human DNA sequence from clone RP3-509L4 on chromosome 6q22.1-22.33
 Contains part of the gene for serologically defined breast cancer
 antigen NY-BR-15 (LOC221312), the PLN gene for phospholamban (PLB),
 a bromodomain-containing 7 (BRD7) pseudogene and a synovial sarcoma
 X breakpoint gene pseudogene, complete sequence.

ACCESSION

VERSION Z99496.1 GI:2780183

KEYWORDS

HTG; BRD7; LOC221312; NY-BR-15; phospholamban; PLB; PLN; SSX.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo

1 (bases 1 to 150290)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
 Clone requests: clonesrequest@sanger.ac.uk

On Jan 16, 1998 this sequence version replaced gi:2578119.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:

Em; EMBL; Sw; SWISSPROT; Tr; TrEMBL; Wp; WORMPEP; Information
 on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
 Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6
 RP3-509L4 is from the library RPCI-3 constructed by the group of

Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm

VECTOR: pCYPAC2

----- Genome Center

Center: Wellcome Trust Sanger Institute

Web site: http://www.sanger.ac.uk

Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one subclone; and the assembly was confirmed by restriction digest,
 except on the rare occasion of the clone being a YAC.

FEATURES

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 NKRSSTLDCKGTFKFSCKEDFRASSSTLRQPDVMTYSALPESKPIWTSSEAPPPK
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QY 121 TGTCTCTTGTGATCTGTATCATCTGTATGCTGCTCTCTGA 159
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Db 64828 TGTCTCTTGTGATCTGTATCATCTGTATGCTGCTCTCTGA 64790
RESULT 13
BD247911
LOCUS BD247911 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV
COMMENT OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503 60/129596 PR
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
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Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCTGTATGCTGCTCTCTGA 159
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Db 121 TGCCTCTTGTGATTTGTCATCATCGTATGCTTCTCTGA 159
RESULT 14
AR302007

LOCUS AR302007 159 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 13 from patent US 6540996.
ACCESSION AR302007
VERSION AR302007.1 GI:31689912
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 13 01-APR-2003;
Devgen NV; Ghent-Zwijnaarde;
GBX;
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Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 159
Db |||||
121 TGCCTCTTGTGATTTGTCATCATCGTATGTTCTCTGA 159
RESULT 15
AX040491
LOCUS AX040491 159 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 13 from Patent WO0063426.
ACCESSION AX040491
VERSION AX040491.1 GI:11230280
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 13 26-OCT-2000;
Devgen NV (BE)
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source Location/Qualifiers
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QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
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Db |||||
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QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGTTCTCTGA 159

Db |||||
121 TGCCTCTTGTGATTTGCAATCATCGTATGCTTCTGA 159
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LOCUS RABPHLAM2 858 bp DNA linear MAM 27-APR-1993
DEFINITION Rabbit phospholamban gene, partial exon 2.
ACCESSION M3601
VERSION M3601.1 GI:165636
KEYWORDS phospholamban.
SEGMENT 2 of 3
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 858)
AUTHORS Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and
MacLennan,D.H.
TITLE Structure of the rabbit phospholamban gene, cloning of the human
cDNA, and assignment of the gene to human chromosome 6
JOURNAL J. Biol. Chem. 266 (18), 11669-11675 (1991)
PUBMED 1828805
COMMENT Original source text: Rabbit DNA.
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
Db |||||
584 CCTCAACAGCAGCTCAAAAGCTCAACCACTTATCAATTTCTGCTCATCTTGA 643
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGTTCTCTGA 159
Db |||||
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RESULT 17
BD247907
LOCUS BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Sus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 159)
Zwaal, R., Groenen, J. and Bogaert, T.
Method for screening compounds
Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV

OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159 /organism='Sus sp. (pig)'.
FT Location/Qualifiers

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DB 121 TGCCTCTTGTGATTTGCATCATCGTGATGCTTCTCTGA 159

RESULT 18
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LOCUS AR302003 159 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9 from patent US 6540996.
ACCESSION AR302003
VERSION AR302003.1 GI:31689908
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 9 01-APR-2003;
DEVGEN NV; Ghent-Zwijnaarde;
GBX; Location/Qualifiers
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Query Match 89.9%; Score 143; DB 6; Length 159;
Best Local Similarity 93.7%; Pred. No. 1.7e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAACTCACTCGCTCAGCTATAGAAGAGCCCTCAACCAATTGAAATG 60
DB 1 ATGGATAAAGTCCAACTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG 60

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 159)
Zwaal, R., Groenen, J. and Bogaert, T.
Method for screening compounds
Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV

OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159 /organism='Sus sp. (pig)'.
FT Location/Qualifiers

FEATURES
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ORIGIN
Query Match 89.9%; Score 143; DB 6; Length 159;
Best Local Similarity 93.7%; Pred. No. 1.7e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAACTCACTCGCTCAGCTATAGAAGAGCCCTCAACCAATTGAAATG 60
DB 1 ATGGATAAAGTCCAACTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAACCTTCAGAACCTTATATCAATTTCTGCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGATCATCGTGATGCTTCTCTGA 159
DB 121 TGCCTCTTGTGATTTGCATCATCGTGATGCTTCTCTGA 159

RESULT 19
AX040487
LOCUS AX040487 159 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 9 from Patent WO0063426.
ACCESSION AX040487
VERSION AX040487.1 GI:11230276
KEYWORDS
SOURCE Sus sp.
ORGANISM Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 9 26-OCT-2000;
DEVGEN NV (BE)

FEATURES
Location/Qualifiers
1..159
/organism='Sus sp.'
/mol_type='unassigned DNA'
/db_xref='taxon:9826'

ORIGIN
Query Match 89.9%; Score 143; DB 6; Length 159;
Best Local Similarity 93.7%; Pred. No. 1.7e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAACTCACTCGCTCAGCTATAGAAGAGCCCTCAACCAATTGAAATG 60
DB 1 ATGGATAAAGTCCAACTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAACCTTCAGAACCTTATATCAATTTCTGCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGATCATCGTGATGCTTCTCTGA 159
DB 121 TGCCTCTTGTGATTTGCATCATCGTGATGCTTCTCTGA 159

RESULT 20
SSPLB
LOCUS SSPLB 737 bp mRNA linear MAM 12-SEP-1993
DEFINITION Pig mRNA for phospholamban.
ACCESSION X15075
VERSION X15075.1 GI:2055
KEYWORDS calcium regulatory protein; phospholamban; transmembrane protein.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 737)
AUTHORS Verboomen, H., Wuyts, F., Eggermont, J. A., De Jaegere, S., Missaen, L., Raeymaekers, L. and Casteels, R.
TITLE cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle
JOURNAL Biochem. J. 262 (1), 353-356 (1989)
PUBMED 2530978
REFERENCE 2 (bases 1 to 737)
AUTHORS Eggermont, J. A.
TITLE Direct Submission

JOURNAL Submitted (13-APR-1999) Eggermont J.A., Laboratorium Voor Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49, B-3000 Leuven, Belgium
COMMENT See <y00399> for canine phospholamban and <y00761> for rabbit phospholamban.
FEATURES Data kindly reviewed (12-OCT-1989) by Eggermont J. A.
source Location/Qualifiers
1..737
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="PLB 7"
/tissue_type="smooth muscle"
/clone_lib="lambda gt11"
/dev_stage="2-day-old piglet"
173..331
/note="unnamed protein product; phospholamban (AA 1-52)"
CDS
1..721
/protein_id="CAA33171.1"
/db_xref="GI:2056"
/db_xref="GOA:P07473"
/db_xref="UniProt/Swiss-Prot:P07473"
/translation="MDKVQYLTRSAIRRASTIEMPQARQLNQLFINFCLILCLLL
ICIIIVMLL"
misc_feature 716..721
/note="pot. polyA signal"
polyA_site 737
/note="polyA site"

ORIGIN

Query Match 89.9%; Score 143; DB 4; Length 2841;
Best Local Similarity 93.7%; Pred. No. 1.4e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAAATG 60
Db |||||
QY 178 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAAATG 237
Db |||||
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 120
Db |||||
QY 238 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 297
Db |||||
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db |||||
QY 298 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 336
Db |||||

RESULT 22

AY514751
LOCUS
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 314)
Housley,D.J.E., Ritzert,E. and Venta,P.J.
Comparative radiation hybrid map of canine chromosome 1
incorporating SNP and indel polymorphisms
Genomics 84 (2), 248-264 (2004)
REFERENCE 2 (bases 1 to 314)
Housley,D.J.E., Ritzert,E. and Venta,P.J.
Direct Submission
Submitted (29-DEC-2003) Small Animal Clinical Sciences and
Microbiology and Molecular Genetics, Michigan State University,
College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES
source Location/Qualifiers
1..314
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/note="sequence information was obtained from a pool of
ten breeds: German shepherd dog; Beagle; German shorthair
pointer; Scottish terrier; Doberman pinscher; Greyhound;
Siberian husky; Labrador retriever; Collie; Cocker
spaniel; additional sequence was obtained from a single
mixed breed dog of unknown origin"
1..>314
/gene="PLN"
<40..>198
/gene="PLN"
/product="phospholamban"
40..198
/gene="PLN"
/codon_start=1

gene

exon

5' UTR

mRNA

CDS

JOURNAL Submitted (13-APR-1999) Eggermont J.A., Laboratorium Voor Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49, B-3000 Leuven, Belgium
COMMENT See <y00399> for canine phospholamban and <y00761> for rabbit phospholamban.
FEATURES Data kindly reviewed (12-OCT-1989) by Eggermont J. A.
source Location/Qualifiers
1..737
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="PLB 7"
/tissue_type="smooth muscle"
/clone_lib="lambda gt11"
/dev_stage="2-day-old piglet"
173..331
/note="unnamed protein product; phospholamban (AA 1-52)"
CDS
1..721
/protein_id="CAA33171.1"
/db_xref="GI:2056"
/db_xref="GOA:P07473"
/db_xref="UniProt/Swiss-Prot:P07473"
/translation="MDKVQYLTRSAIRRASTIEMPQARQLNQLFINFCLILCLLL
ICIIIVMLL"
misc_feature 716..721
/note="pot. polyA signal"
polyA_site 737
/note="polyA site"

ORIGIN

Query Match 89.9%; Score 143; DB 4; Length 737;
Best Local Similarity 93.7%; Pred. No. 1.4e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAAATG 60
Db |||||
QY 173 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAAATG 232
Db |||||
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 120
Db |||||
QY 233 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 292
Db |||||
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db |||||
QY 293 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 331
Db |||||

RESULT 21

OCPLAM
LOCUS
DEFINITION O. cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:1661
KEYWORDS
SOURCE Phospholamban.
ORGANISM Oryctolagus cuniculus (rabbit)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
Fuji,J., Lytton,J., Tada,M. and MacLennan,D.H.
Rabbit cardiac and slow-twitch muscle express the same
phospholamban gene
FEBS Lett. 227 (1), 51-55 (1988)
JOURNAL PUBLISHED 2962883
FEATURES
source Location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"

gene

exon

5' UTR

mRNA

CDS

3'UTR
ICIVMLL
391..>669
/gene="PLN"
ORIGIN
Query Match 87.9%; Score 139.8; DB 4; Length 314;
Best Local Similarity 92.5%; Pred. No. 1.1e-26;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCATTTGAAATG 60
Db 40 ATGGATAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCTTCAACCATTTGAAATG 99
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATTCAATTTCTGTCTCATCTTAATA 120
Db 100 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATATAAATTTCTGTCTCATTTAATA 159
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 160 TGTCTCTTGTGATCTGTATCATCTTGTGATGCTTCTCTGA 198
RESULT 23
AY576871S2 669 bp DNA linear MAM 01-APR-2005
LOCUS Canis familiaris phospholamban (PLN) gene, exon 2 and complete cds.
DEFINITION Canis familiaris phospholamban (PLN) gene, exon 2 and complete cds.
ACCESSION AY576872
VERSION AY576872.1 GI:48996075
KEYWORDS
SEGMENT 2 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 669)
Stabej, P., Leegwater, P.A., Stokhof, A.A. and van Oost, B.A.
Evaluation of the phospholamban gene in purebred dogs with dilated
cardiomyopathy
Unpublished
REFERENCE 2 (bases 1 to 669)
Stabej, P., Leegwater, P.A. and van Oost, B.A.
Direct Submission
Submitted (19-MAR-2004) Clinical Sciences of Companion Animals,
Utrecht University, Yalelaan 8, Utrecht 3584CM, The Netherlands
FEATURES
source
1..669
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/chromosome="1"
/notes="breed: Doberman"
order(AY576871.1:1..438,1..>669)
/gene="PLN"
join(AY576871.1:201..283,131..>669)
/gene="PLN"
/product="phospholamban"
join(AY576871.1:201..283,131..231)
/gene="PLN"
131..>669
/gene="PLN"
/number=2
232..390
/gene="PLN"
/codon_start=1
/product="phospholamban"
/protein_id="AA748602.1"
/db_xref="GI:48996076"
/translation="MDKVQYLTRSAIRRASTIEMPOQARQLNQLNFNCLILICLLL

3'UTR
ICIVMLL
391..>669
/gene="PLN"
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Query Match 87.9%; Score 139.8; DB 4; Length 669;
Best Local Similarity 92.5%; Pred. No. 9.9e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCATTTGAAATG 60
Db 232 ATGGATAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCTTCAACCATTTGAAATG 291
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATTCAATTTCTGTCTCATCTTAATA 120
Db 232 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATATAAATTTCTGTCTCATTTAATA 351
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 352 TGTCTCTTGTGATCTGTATCATCTTGTGATGCTTCTCTGA 390
RESULT 24
DOGPHL 832 bp mRNA linear MAM 27-APR-1993
LOCUS Canine cardiac phospholamban mRNA.
DEFINITION M16012
ACCESSION M16012.1 GI:164043
VERSION phospholamban.
KEYWORDS Canis lupus (gray wolf)
SOURCE Canis lupus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 832)
Fujii, J., Ueno, A., Kitano, K., Tanaka, S., Kadoya, M. and Tada, M.
Complete complementary DNA-derived amino acid sequence of canine
cardiac phospholamban
J. Clin. Invest. 79 (1), 301-304 (1987)
3793929
COMMENT Original source text: Dog cDNA to mRNA.
FEATURES
source
1..832
/organism="Canis lupus"
/mol_type="mRNA"
/db_xref="taxon:9612"
181..339
/note="cardiac phospholamban"
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/protein_id="AAA30884.1"
/db_xref="GI:164044"
/translation="MDKVQYLTRSAIRRASTIEMPOQARQLNQLNFNCLILICLLL
ICIVMLL"
ORIGIN
Query Match 87.9%; Score 139.8; DB 4; Length 832;
Best Local Similarity 92.5%; Pred. No. 9.6e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCATTTGAAATG 60
Db 181 ATGGATAAAGTCCCAATACCTCACTCGCTCAGCTATAGAAGAGCTTCAACCATTTGAAATG 240
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATTCAATTTCTGTCTCATCTTAATA 120
Db 241 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATATAAATTTCTGTCTCATTTAATA 300
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 301 TGTCTCTTGTGATCTGTATCATCTTGTGATGCTTCTCTGA 339
RESULT 25

DOGFLBA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DOG cardiac phospholamban mRNA, complete cds.
M35393.1 GI:164045
phospholamban.
Canis sp.
Canis sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

1 (bases 1 to 832)
Uyeda.A., Kitano.K., Fujii.J., Kadoma.M., Tada.M. and Tanaka.S.
Characterization of recombinant cDNA clones for canine cardiac
phospholamban
Nucleic Acids Symp. Ser. 17, 121-124 (1986)
3562256
COMMENT
FEATURES

Original source text: Dog heart, cDNA to mRNA, clone pPLB1.
Location/Qualifiers
1..832
/organism="Canis sp."
/mol_type="mRNA"
/db_xref="taxon:9616"
181..339
/note="cardiac phospholamban (EC 2.7.1.37)"
/codon_start=1
/protein_id="AAC41618.1"
/db_xref="GI:164045"
/translation="MDKVQLYTRSAIRRASTIEMPPQARQLNQLFINFCLILCLLL
ICIIIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 832;
Best Local Similarity 92.5%; Pred. No. 9.6e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 60
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DB 181 ATGGATAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 240
|||||

QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
|||||
DB 241 CCTCAACAGCAGTCAAAATCTTCAGAACCTATTATAAATTTCTGCTCATTTAATA 300
|||||

QY 121 TGTCTCTTGTGATCTGATCATCGTCATGCTCTCTGA 159
|||||
DB 301 TGTCTCTTGTGATCTGATCATCTGATGCTCTCTGA 339
|||||

RESULT 26
CFPHLX
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Dog phospholamban mRNA, complete cds.
Y00399.1 GI:911
phospholamban.
Canis familiaris (dog)
Canis familiaris
Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

1 (bases 1 to 2614)
Uyeda.A., Kitano.K., Fujii.J., Kadoma.M., Tada.M. and Tanaka.S.
The cDNA sequence of the major phospholamban mRNA in canine cardiac
ventricular muscle
Nucleic Acids Res. 15 (16), 6738 (1987)
3628007
COMMENT
FEATURES

Location/Qualifiers
1..2614
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
185..343

CDS

DOGFLBA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Dog cardiac phospholamban mRNA, complete cds.
M35393.1 GI:164045
phospholamban.
Canis sp.
Canis sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

1 (bases 1 to 832)
Uyeda.A., Kitano.K., Fujii.J., Kadoma.M., Tada.M. and Tanaka.S.
Characterization of recombinant cDNA clones for canine cardiac
phospholamban
Nucleic Acids Symp. Ser. 17, 121-124 (1986)
3562256
COMMENT
FEATURES

Original source text: Dog heart, cDNA to mRNA, clone pPLB1.
Location/Qualifiers
1..832
/organism="Canis sp."
/mol_type="mRNA"
/db_xref="taxon:9616"
181..339
/note="cardiac phospholamban (EC 2.7.1.37)"
/codon_start=1
/protein_id="AAC41618.1"
/db_xref="GI:164045"
/translation="MDKVQLYTRSAIRRASTIEMPPQARQLNQLFINFCLILCLLL
ICIIIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 832;
Best Local Similarity 92.5%; Pred. No. 9.6e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 60
|||||
DB 181 ATGGATAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 240
|||||

QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
|||||
DB 241 CCTCAACAGCAGTCAAAATCTTCAGAACCTATTATAAATTTCTGCTCATTTAATA 300
|||||

QY 121 TGTCTCTTGTGATCTGATCATCGTCATGCTCTCTGA 159
|||||
DB 301 TGTCTCTTGTGATCTGATCATCTGATGCTCTCTGA 339
|||||

RESULT 26
CFPHLX
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Dog phospholamban mRNA, complete cds.
Y00399.1 GI:911
phospholamban.
Canis familiaris (dog)
Canis familiaris
Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

1 (bases 1 to 2614)
Uyeda.A., Kitano.K., Fujii.J., Kadoma.M., Tada.M. and Tanaka.S.
The cDNA sequence of the major phospholamban mRNA in canine cardiac
ventricular muscle
Nucleic Acids Res. 15 (16), 6738 (1987)
3628007
COMMENT
FEATURES

Location/Qualifiers
1..2614
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
185..343

CDS

/note="unnamed protein product; phospholamban"
/codon_start=1
/protein_id="CAA68461.1"
/db_xref="GI:912"
/db_xref="GOA:P61012"
/db_xref="InterPro:IPR005984"
/db_xref="UniProt/SwissProt:P61012"
/translation="MDKVQLYTRSAIRRASTIEMPPQARQLNQLFINFCLILCLLL
ICIIIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 2614;
Best Local Similarity 92.5%; Pred. No. 8.1e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 60
|||||
DB 185 ATGGATAAAGTCCAAATACCTCAGCTGCTATAGAGAGAGCTCAACCAATGAAATG 244
|||||

QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
|||||
DB 245 CCTCAACAGCAGTCAAAATCTTCAGAACCTATTATAAATTTCTGCTCATTTAATA 304
|||||

QY 121 TGTCTCTTGTGATCTGATCATCGTCATGCTCTCTGA 159
|||||
DB 305 TGTCTCTTGTGATCTGATCATCTGATGCTCTCTGA 343
|||||

RESULT 27
AC013809
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens clone RP11-21C18, LOW-PASS SEQUENCE SAMPLING.
AC013809
AC013809.4 GI:9123984
HTGS PHASRO.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 179556)
Birren.B., Linton.L., Nusbaum.C. and Lander.E.
Homo sapiens, clone RP11-21C18
Unpublished
2 (bases 1 to 179556)
Birren.B., Linton.L., Nusbaum.C., Lander.E., Allen.N., Anderson.M.,
Baldwin.J., Barna.N., Beckerly.R., Boguslavsky.L., Boukhgalter.B.,
Brown.A., Castle.A., Colangelo.M., Collins.S., Collymore.A.,
Cooke.P., DeArelano.K., Dewar.K., Domino.M., Donegan.L., Doyle.M.,
Ferreira.P., Fitzhugh.W., Forrest.C., Funke.R., Gage.D.,
Galligan.J., Gardyna.S., Grant.G., Hagos.B., Heaford.A., Horton.L.,
Howland.J.C., Johnson.R., Jones.C., Kann.L., Karatas.A., Klein.J.,
Lehoczky.J., Lieu.C., Locke.K., Macdonald.P., Marquis.N.,
McEwan.P., McGurk.A., McKernan.K., McLaughlin.J., Meldrim.J.,
Morrow.J., Naylor.J., Norman.C.H., O'Connor.T., O'Donnell.P.,
Peterson.K., Pollara.V., Riley.R., Roy.A., Santos.R., Severy.P.,
Stange-Thomann.N., Stojanovic.N., Subramanian.A., Talamas.J.,
Testaye.S., Tirrell.A., Vassiliev.H., Vo.A., Wheeler.J., Wu.X.,
Wyman.D., Ye.W.J., Zimmer.A. and Zody.M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:7107985.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3976

Center clone name: 21_C_18

* NOTE: This record contains 191 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 780: contig of 780 bp in length
781 880: gap of 100 bp
881 1631: contig of 751 bp in length
1632 1731: gap of 100 bp
1732 2490: contig of 759 bp in length
2491 2590: gap of 100 bp
2591 3363: contig of 773 bp in length
3364 3463: gap of 100 bp
3464 4235: contig of 772 bp in length
4236 4335: gap of 100 bp
4336 5117: contig of 782 bp in length
5118 6006: contig of 789 bp in length
6007 6106: gap of 100 bp
6107 6869: contig of 763 bp in length
6870 6969: gap of 100 bp
6970 7733: contig of 764 bp in length
7734 8607: contig of 774 bp in length
8608 8707: gap of 100 bp
8708 9479: contig of 772 bp in length
9480 9579: gap of 100 bp
9580 10344: contig of 765 bp in length
10345 10444: gap of 100 bp
10445 11212: contig of 768 bp in length
11213 12066: contig of 754 bp in length
12067 12166: gap of 100 bp
12167 12972: contig of 806 bp in length
12973 13072: gap of 100 bp
13073 13842: contig of 770 bp in length
13843 13942: gap of 100 bp
13944 14708: contig of 766 bp in length
14709 14808: gap of 100 bp
14809 15579: contig of 771 bp in length
15580 15679: gap of 100 bp
15680 16450: contig of 771 bp in length
16451 16550: gap of 100 bp
16551 17324: contig of 774 bp in length
17325 17424: gap of 100 bp
17425 18199: contig of 775 bp in length
18200 18299: gap of 100 bp
18300 19041: contig of 742 bp in length
19042 19141: gap of 100 bp
19142 19940: contig of 799 bp in length
19941 20040: gap of 100 bp
20041 20792: contig of 752 bp in length
20793 20892: gap of 100 bp
20893 21652: contig of 760 bp in length
21653 21752: gap of 100 bp
21753 22531: contig of 779 bp in length
22532 22631: gap of 100 bp
22632 23404: contig of 773 bp in length
23405 23504: gap of 100 bp
23505 24283: contig of 779 bp in length
24284 24383: gap of 100 bp
24384 25152: contig of 769 bp in length
25153 25252: gap of 100 bp
25253 26020: contig of 768 bp in length
26021 26120: gap of 100 bp

26121 26894: contig of 774 bp in length
26895 26994: gap of 100 bp
26995 27757: contig of 763 bp in length
27758 27857: gap of 100 bp
27858 28638: contig of 781 bp in length
28639 28738: gap of 100 bp
28739 29512: contig of 774 bp in length
29513 29612: gap of 100 bp
29613 30394: contig of 782 bp in length
30395 30494: gap of 100 bp
30495 31270: contig of 776 bp in length
31271 31370: gap of 100 bp
31371 32140: contig of 770 bp in length
32141 32240: gap of 100 bp
32241 33008: contig of 768 bp in length
33009 33108: gap of 100 bp
33109 33891: contig of 783 bp in length
33892 33991: gap of 100 bp
33992 34774: contig of 783 bp in length
34775 34874: gap of 100 bp
34875 35638: contig of 764 bp in length
35639 35738: gap of 100 bp
35739 36511: contig of 773 bp in length
36512 36612: gap of 100 bp
36612 37381: contig of 770 bp in length
37382 37481: gap of 100 bp
37482 38270: contig of 789 bp in length
38271 38370: gap of 100 bp
38371 39151: contig of 781 bp in length
39152 39251: gap of 100 bp
39252 40022: contig of 771 bp in length
40023 40122: gap of 100 bp
40123 40894: contig of 772 bp in length
40895 40994: gap of 100 bp
40995 41765: contig of 771 bp in length
41766 41865: gap of 100 bp
41866 42619: contig of 754 bp in length
42620 42719: gap of 100 bp
42720 43503: contig of 784 bp in length
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43604 44367: contig of 764 bp in length
44368 44467: gap of 100 bp
44468 45241: contig of 774 bp in length
45242 45341: gap of 100 bp
45342 46113: contig of 772 bp in length
46114 46213: gap of 100 bp
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47848 47947: gap of 100 bp
47948 48720: contig of 773 bp in length
48721 48820: gap of 100 bp
48821 49593: contig of 773 bp in length
49594 49693: gap of 100 bp
49694 50493: contig of 800 bp in length
50494 50593: gap of 100 bp
50594 51359: contig of 766 bp in length
51360 51459: gap of 100 bp
51460 52244: contig of 785 bp in length
52245 52344: gap of 100 bp
52345 53132: contig of 788 bp in length
53133 53232: gap of 100 bp
53233 53993: contig of 761 bp in length
53994 54093: gap of 100 bp
54094 54863: contig of 770 bp in length
54864 54963: gap of 100 bp
54964 55732: contig of 769 bp in length
55733 55832: gap of 100 bp
55833 56605: contig of 773 bp in length
56606 56705: gap of 100 bp
56706 57460: contig of 755 bp in length
57461 57560: gap of 100 bp
57561 58365: contig of 805 bp in length

REFERENCE	Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 940) Ganim,U.R., Luo,W., Ponniah,S., Grupp,I., Kim,H.W., Ferguson,D.G., Kadambi,V., Neumann,J.C., Doetschman,T. and Kranias,E.G.
TITLE	Mouse phospholamban gene expression during development in vivo and in vitro
JOURNAL	Circ. Res. 71 (5), 1021-1030 (1992)
PUBMED	1394867
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gisbqz 116999] from the original journal article.
FEATURES	<p>Location/Qualifiers</p> <p>1..940</p> <p>/organism="Mus sp."</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:10095"</p> <p>1..940</p> <p>/gene="phospholamban"</p> <p>181..339</p> <p>/gene="phospholamban"</p> <p>/codon_start=1</p> <p>/product="phospholamban"</p> <p>/protein_id="AAB23706.1"</p> <p>/db_xref="GI:257746"</p> <p>/translation="MEKQYLTRSAIRRASTIEMPOQARQLQNLFINCLILICLL ICIIWML"</p>
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Best Local Similarity	88.1%; Pred. No. 8.9e-24;
Matches 140; Conservative	0; Mismatches 19; Indels 0; Gaps 0;
QY	1 ATGCGAAGAGTCATACCTCACTCGCTCAGCTATAGAAGAGCTCAACATTGAATG 60
Db	181 ATGGAAGAGTGAATACCTCACTCGCTCGCTATCAGAGAGCTCATTGAATG 240
QY	61 CCTCAAGACGCTCAAAAGCTCAGCAATCTATTATCAATTTCTGCTCATTTAATA 120
Db	241 CCTCAGCAGCAGCTCAGCAATCTCAGAACCTATTATCAATTTCTGCTCATTTGATA 300
QY	121 TGTCTCTGCTGATCTGATCATCTGCTGATGCTCTCTGA 159
Db	301 TGTCTCTGCTGATCTGATCATCTGCTGATGCTCTCTGTA 339
RESULT 30	AC153524
LOCUS	Mus musculus 10 BAC RP23-349H12 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence.
DEFINITION	AC153524 AC099716
ACCESSION	AC153524.3 GI:58197576
VERSION	HTG.
KEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 167574) Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I., Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K., Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T., Gaskin,C., Gensch,S., Ghose,S., Gill,R., Gonzalez,D., Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeberlen,K., Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Haviak,P.,

Qy 1 ATGGAAGAGTCCATACCTCACTCGCTCAGCTATAGAGAGGCTCAACCATTTGAATG 60
Db 127 ATGGAAGAGTCCATACCTCACTCGCTCAGCTATAGAGAGGCTCAACCATTTGAATG 186
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 187 CCTCAGCAGCAGCTCAGAAATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGA 246
Qy 121 TGTCTCTTGTGATCTGATCATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 159
Db 247 TGTCTCTTGTGATCTGATCATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 285

RESULT 32
AC100317
LOCUS Mus musculus clone RP23-124E8, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC100317
ACCESSION AC100317.1 GI:17047683
VERSION HTG; HTGS PHASE0.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 79895)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE Mus musculus, clone RP23-124E8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 79895)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhaltier,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliiev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lakocque,K.,
Lamazzares,R., Landers,T., Lehotzky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., O'Neil,D.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., Pollara,V.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W18R
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15083
Center clone name: 124_E_8

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 986: contig of 986 bp in length
987 1086: gap of 100 bp
1087 1937: contig of 851 bp in length
1938 2037: gap of 100 bp
2038 3001: contig of 964 bp in length
3002 3101: gap of 100 bp
3102 4053: contig of 952 bp in length
4054 4153: gap of 100 bp
4154 5121: contig of 968 bp in length
5122 6182: contig of 961 bp in length
6183 7234: contig of 952 bp in length
7235 7334: gap of 100 bp
7335 8357: contig of 1023 bp in length
8358 9464: contig of 1007 bp in length
9465 10584: contig of 1020 bp in length
10585 10684: gap of 100 bp
10686 11702: contig of 1018 bp in length
11703 11802: gap of 100 bp
11804 12769: contig of 967 bp in length
12770 12869: gap of 100 bp
12870 13335: contig of 966 bp in length
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21353 22407: contig of 955 bp in length
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23481 23580: gap of 100 bp
23581 24553: contig of 973 bp in length
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26848 27857: contig of 1010 bp in length
27858 27957: gap of 100 bp
27959 28963: contig of 1006 bp in length
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29064 30073: contig of 1010 bp in length
30074 30173: gap of 100 bp
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31123 31222: gap of 100 bp
31223 32192: contig of 970 bp in length
32193 32292: gap of 100 bp
32293 33178: contig of 886 bp in length
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33279 34290: contig of 1012 bp in length
34291 34390: gap of 100 bp
34391 35386: contig of 996 bp in length
35387 35486: gap of 100 bp
35487 36494: contig of 1008 bp in length
36495 36594: gap of 100 bp

36595 37579: contig of 985 bp in length
37580 37679: gap of 100 bp
37680 38692: contig of 1013 bp in length
38692 38792: gap of 100 bp
38792 39797: contig of 1005 bp in length
39797 39897: gap of 100 bp
39897 40757: contig of 860 bp in length
40757 40857: gap of 100 bp
40857 41873: contig of 1016 bp in length
41873 41973: gap of 100 bp
41973 42930: contig of 957 bp in length
42930 43030: gap of 100 bp
43030 43983: contig of 953 bp in length
43983 44083: gap of 100 bp
44083 45016: contig of 933 bp in length
45016 45116: gap of 100 bp
45116 46104: contig of 988 bp in length
46104 46204: gap of 100 bp
46204 47220: contig of 1016 bp in length
47220 47320: gap of 100 bp
47320 48316: contig of 996 bp in length
48316 48416: gap of 100 bp
48416 49421: contig of 1005 bp in length
49421 49521: gap of 100 bp
49521 50475: contig of 954 bp in length
50475 50575: gap of 100 bp
50575 51526: contig of 951 bp in length
51526 51626: gap of 100 bp
51626 52563: contig of 937 bp in length
52563 52663: gap of 100 bp
52663 53648: contig of 985 bp in length
53648 53748: gap of 100 bp
53748 54722: contig of 974 bp in length
54722 54822: gap of 100 bp
54822 55838: contig of 1016 bp in length
55838 55938: gap of 100 bp
55938 56910: contig of 972 bp in length
56910 57010: gap of 100 bp
57010 57967: contig of 957 bp in length
57967 58067: gap of 100 bp
58067 59079: contig of 1012 bp in length
59079 59179: gap of 100 bp
59179 60170: contig of 991 bp in length
60170 60270: gap of 100 bp
60270 61301: contig of 1031 bp in length
61301 61401: gap of 100 bp
61401 62461: contig of 1060 bp in length
62461 62561: gap of 100 bp
62561 63533: contig of 972 bp in length
63533 63633: gap of 100 bp
63633 64591: contig of 958 bp in length
64591 64691: gap of 100 bp
64691 65673: contig of 982 bp in length
65673 65773: gap of 100 bp
65773 66768: contig of 995 bp in length
66768 67821: contig of 953 bp in length
67821 67921: gap of 100 bp
67921 68923: contig of 1002 bp in length
68923 69023: gap of 100 bp
69023 70050: contig of 1027 bp in length
70050 70150: gap of 100 bp
70150 71165: contig of 1015 bp in length
71165 71265: gap of 100 bp
71265 72235: contig of 970 bp in length
72235 72335: gap of 100 bp
72335 73360: contig of 1025 bp in length
73360 73460: gap of 100 bp
73460 74414: contig of 954 bp in length
74414 79.9%: Score 127; DB 14; Length 79895;
Best Local Similarity 87.4%; Pred. No. 1.3e-23;
Matches 139; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1 ATGGAGAAAGTCCCAATACCTCAGCTCGCTAGCTATAGAGAGCTCAACCAATTGAAATG 60
78979 ATGGAATAAGTGAATACCTCAGCTCGCTCGCTATCAGGAGAGCTCCCACTATTGAAATG 79038
61 CCTCAACAAGCACGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
79039 CCTCAGCAGCAGCTGAGATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGATA 79098
121 TGTCTCTTGTGATCTGCTATCATCGTATGATGCTTCTCTGA 159
79099 TGTCTGCTGATCTGCTATCATCATGATGATGCTTCTGTA 79137

RESULT 33
S95853
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Rattus sp.
phospholamban [rate, aortic smooth muscle, mRNA, 159 nt].
S95853
S95853.1 GI:247932
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 159)
Hwang, K.S. and Nadal-Ginard, B.
TITLE
Cloning phospholamban cDNA from rat aortic smooth muscle
JOURNAL
Adv. Exp. Med. Biol. 304, 387-395 (1991)
PUBMED
1725098
REMARK
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsg 95853] from the original journal article.

FEATURES
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Query Match 78.9%; Score 125.4; DB 9; Length 159;
Best Local Similarity 86.8%; Pred. No. 8.2e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

1 ATGGAGAAAGTCCCAATACCTCAGCTCGCTAGCTATAGAGAGCTCAACCAATTGAAATG 60
78979 ATGGAATAAGTGAATACCTCAGCTCGCTCGCTATCAGGAGAGCTCCCACTATTGAAATG 79038
61 CCTCAACAAGCACGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
79039 CCTCAGCAGCAGCTGAGATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGATA 79098
121 TGTCTCTTGTGATCTGCTATCATCGTATGATGCTTCTCTGA 159
79099 TGTCTGCTGATCTGCTATCATCATGATGATGCTTCTGTA 79137

RESULT 34
S95849
LOCUS
DEFINITION
ACCESSION
Rattus sp. phospholamban (Pin) mRNA, complete cds.
S95849

36595 37579: contig of 985 bp in length
37580 37679: gap of 100 bp
37680 38692: contig of 1013 bp in length
38692 38792: gap of 100 bp
38792 39797: contig of 1005 bp in length
39797 39897: gap of 100 bp
39897 40757: contig of 860 bp in length
40757 40857: gap of 100 bp
40857 41873: contig of 1016 bp in length
41873 41973: gap of 100 bp
41973 42930: contig of 957 bp in length
42930 43030: gap of 100 bp
43030 43983: contig of 953 bp in length
43983 44083: gap of 100 bp
44083 45016: contig of 933 bp in length
45016 45116: gap of 100 bp
45116 46104: contig of 988 bp in length
46104 46204: gap of 100 bp
46204 47220: contig of 1016 bp in length
47220 47320: gap of 100 bp
47320 48316: contig of 996 bp in length
48316 48416: gap of 100 bp
48416 49421: contig of 1005 bp in length
49421 49521: gap of 100 bp
49521 50475: contig of 954 bp in length
50475 50575: gap of 100 bp
50575 51526: contig of 951 bp in length
51526 51626: gap of 100 bp
51626 52563: contig of 937 bp in length
52563 52663: gap of 100 bp
52663 53648: contig of 985 bp in length
53648 53748: gap of 100 bp
53748 54722: contig of 974 bp in length
54722 54822: gap of 100 bp
54822 55838: contig of 1016 bp in length
55838 55938: gap of 100 bp
55938 56910: contig of 972 bp in length
56910 57010: gap of 100 bp
57010 57967: contig of 957 bp in length
57967 58067: gap of 100 bp
58067 59079: contig of 1012 bp in length
59079 59179: gap of 100 bp
59179 60170: contig of 991 bp in length
60170 60270: gap of 100 bp
60270 61301: contig of 1031 bp in length
61301 61401: gap of 100 bp
61401 62461: contig of 1060 bp in length
62461 62561: gap of 100 bp
62561 63533: contig of 972 bp in length
63533 63633: gap of 100 bp
63633 64591: contig of 958 bp in length
64591 64691: gap of 100 bp
64691 65673: contig of 982 bp in length
65673 65773: gap of 100 bp
65773 66768: contig of 995 bp in length
66768 67821: contig of 953 bp in length
67821 67921: gap of 100 bp
67921 68923: contig of 1002 bp in length
68923 69023: gap of 100 bp
69023 70050: contig of 1027 bp in length
70050 70150: gap of 100 bp
70150 71165: contig of 1015 bp in length
71165 71265: gap of 100 bp
71265 72235: contig of 970 bp in length
72235 72335: gap of 100 bp
72335 73360: contig of 1025 bp in length
73360 73460: gap of 100 bp
73460 74414: contig of 954 bp in length
74414 79.9%: Score 127; DB 14; Length 79895;
Best Local Similarity 87.4%; Pred. No. 1.3e-23;
Matches 139; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1 ATGGAGAAAGTCCCAATACCTCAGCTCGCTAGCTATAGAGAGCTCAACCAATTGAAATG 60
78979 ATGGAATAAGTGAATACCTCAGCTCGCTCGCTATCAGGAGAGCTCCCACTATTGAAATG 79038
61 CCTCAACAAGCACGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
79039 CCTCAGCAGCAGCTGAGATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGATA 79098
121 TGTCTCTTGTGATCTGCTATCATCGTATGATGCTTCTCTGA 159
79099 TGTCTGCTGATCTGCTATCATCATGATGATGCTTCTGTA 79137

RESULT 34
S95849
LOCUS
DEFINITION
ACCESSION
Rattus sp. phospholamban (Pin) mRNA, complete cds.
S95849

VERSION	S95849.1	GI:247934	
KEYWORDS	Rattus sp.		
SOURCE	Rattus sp.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 386)		
AUTHORS	Hwang,K.S. and Nadal-Ginard,B.		
TITLE	Cloning phospholamban cDNA from rat aortic smooth muscle		
JOURNAL	Adv. Exp. Med. Biol. 304, 387-395 (1991)		
PUBMED	1725098		
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbet 95849] from the original journal article. This sequence comes from Fig.2.		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:10118"		
gene	1..386		
	/tissue_type="cardiac smooth muscle"		
	/gene="Pln"		
CDS	159..317		
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	/codon_start=1		
	/product="phospholamban"		
	/protein_id="AA086727.1"		
	/db_xref="GI:26986719"		
	/translation="MEKVQLTRSAIRRASTIEMPPQARQLNQLFINFCLILCLLL		
	ICIIIVMLL"		
ORIGIN			
Query Match	78.9%;	Score 125.4;	DB 9; Length 386;
Best Local Similarity	86.8%;	Pred. No. 7.2e-23;	
Matches 138;	Conservative 0;	Mismatches 21;	Indels 0; Gaps 0;
QY	1	ATGGAGAAAGTCCAAATACCTCACTCGCTACGCTATAGAGAGCGCTCAACCATTTGAAATG	60
Db	814	ATGGAAAAAGTCCAAATACCTTACTCGCTCGGTATCAGAGAGCGCTCGACTATTGAAATG	873
QY	61	CCTCAACAGCAGCGTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA	120
Db	874	CCCCAGACGCGGTCAAGACCTCCAGAACCTTTTATCAATTTCTGCTCATCTTGATA	933
QY	121	TGTCCTTGTGATCTGTATCATCGTATCGTCTCTCTGA	159
Db	934	TGTCCTGCTGATCTGCATCATCTGTGATCTTCTGTGA	972
RESULT 35			
LOCUS	AC097906	223728 bp	DNA linear HTG 10-MAY-2003
DEFINITION	Rattus norvegicus clone CH230-147118, WORKING DRAFT SEQUENCE.		
ACCESSION	AC097906		
VERSION	AC097906.7	GI:30520963	
KEYWORDS	HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 223728)		
AUTHORS	Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Cavazos,I., Caesar,H., Chen,Z., Chou,J., Cardenas,V., Carter,K., Cavazos,I., Chen,R., Chen,Y., Chen,Z., Chu,J., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chou,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,		

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Loubege, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahoney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montanayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, J., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Rives, C., Rodkey, T., Roy, Y., Reuter, M., Richards, S., Riggs, F., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlecyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

TITLE
JOURNAL

REFERENCE
AUTHORS

TITLE
JOURNAL

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

Unpublished
2 (bases 1 to 223728)
Worley, K. C.

Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 223728)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24942703.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GFOK

Center clone name: CH230-147118

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 210120 bases at least Q40

Consensus quality: 212963 bases at least Q30

Consensus quality: 214568 bases at least Q20

Estimated insert size: 220584; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 223728: contig of 223728 bp in length.

FEATURES
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1. 223728

/organism="Rattus norvegicus"

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/db_xref="taxon:10116"

/clone="CH230-147118"

1. 995

/note="wgs contig"

complement(217014..217851)

/note="clone boundary"

clone end:T7

site:ECORI

end_sequence:RWBAJ57TJB"

ORIGIN

Query Match 78.9%; Score 125.4; DB 14; Length 223728;

Best Local Similarity 86.8%; Pred. No. 2.9e-23;

Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGAGAAAGTCCAAATACCTCCTCGCTATGAGAGAGCTCAACCATTTGAATG 60

Db 82163 ATGAGAAAGTCCAAATACCTCCTCGCTATGAGAGAGCTCAACCATTTGAATG 82222

Qy 61 CCTCACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120

Db 82223 CCCAGCAAGCGCTCAGAACTCCAGAACCTCTTTATCAATTTCTCTCATCTTGATA 82282

Qy 121 TGTCTCTTGTGATCTGTCATCATCGTATGATCTCTCTGA 159

Db 82283 TGTCTCTTGTGATCTGTCATCATCGTATGATCTCTCTGA 82321

RESULT 37

LOCUS

AC128365/c

DEFINITION

Rattus norvegicus clone CH230-46019, WORKING DRAFT SEQUENCES, 2

unordered pieces.

AC128365

AC128365.5 GI:25007909

VERSION

HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Rattus.

1 (bases 1 to 231910)

Muzny, D., Marie, Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, Z., Chu, J.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Frederick, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Hagland, W., Hamil, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpthy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lohenshuwa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newcon,N., Nguyen,N., Norris,S., Nwaokemeleah,O., Okwuonu,G., Olarnpungagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfankoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sigson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Uemami,K., Velas,R., Vera,V., Villasanad,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczkyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 231910)
Worley,K.C.

Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 231910)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23265008.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZBY
Center clone name: CH230-46019
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 226527 bases at least Q40
Consensus quality: 227741 bases at least Q30
Consensus quality: 228571 bases at least Q20
Estimated insert size: 231458; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 230788: contig of 230788 bp in length
* 230789 230888: gap of unknown length
* 230889 231910: contig of 1022 bp in length.

FEATURES
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site:
end sequence:BH332000"
complement(224996..225875)
/note="clone boundary
clone_end:Sp6"
site:
end sequence:BH332001"
227746..230788
/note="wgs end extension
clone_end:Sp6"
230789..230888
/estimated_length=unknown

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gap

ORIGIN
Query Match 78.9%; Score 125.4; DB 14; Length 231910;
Best Local Similarity 86.8%; Pred. No. 2.9e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAATACCTCTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
57561 ATGGAGAAAGTCCAATACCTCTCTCGCTCAGCTATTAAGAGAGCCTCGACTATTGAATG 57502
QY 61 CCTCAACAGCAGCTCAAGAGTACAGATCTATTATCAATTTCTCTCATCTTAATA 120
57501 CCCAGCAGCGCGTCCAGAACCTCCAGAACCTCTTTATCAATTTCTCTCATCTTGA 57442
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTGCTTCTCTGA 159
57441 TGTCTCTTGTGATCTGTATCATCGTGTGCTTCTCTGA 57403

RESULT 38
RNPFLAMB
LOCUS RNPFLAMB 701 bp mRNA linear ROD 18-APR-2005
DEFINITION R.norvegicus mRNA for phospholamban.
ACCESSION X71068
VERSION X71068.1 GI:313809
KEYWORDS phospholamban.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
Shanahan,C.M., Weissberg,P.L. and Metcalfe,J.C.
Isolation of gene markers of differentiated and proliferating
vascular smooth muscle cells
Circ. Res. 73 (1), 193-204 (1993)
JOURNAL

```

8508530
2 (bases 1 to 701)
AUTHORS
  Shanahan,C.M.
TITLE
  Direct Submission
JOURNAL
  Submitted (26-FEB-1993) C.M. Shanahan, University of Cambridge,
  Dept of Biochemistry, Tennis Court Road, Cambridge CB2 1QW, UK
FEATURES
  source
    Location/Qualifiers
      1..701
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        /clone="2RB7"
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        /clone_lib="lambda-Zap"
        /dev_stage="adult"
        174..332
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          /product="phospholamban"
          /protein_id="CAA50394.1"
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          /db_xref="GOA:P61016"
          /db_xref="InterPro:IPR005984"
          /db_xref="UniProt/Swiss-Prot:P61016"
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          ICIVMLL"

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Best Local Similarity 86.24; Pred. No. 1.8e-22;
Matches 137; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
    |||||
Db 174 ATGGAANAAGTCANATACCTTACTCGCTCGGCTATTAGGAGAGCCTCGACTATTGAAATG 233
    |||||

QY 61 CCTCAACAAGCAGCTCAAAGCTACAGATCTATTTATCAATTTCTGTCATCTTAATA 120
    |||||
Db 234 CCCAGCAAGCGCGTTCAGAACCTCCAGAACCTTTATCAATTTCTGTCATCTTAATA 293
    |||||

QY 121 TGTCTCTTGTGATCTGATCATCATCGTGATGCTTCTCTGA 159
    |||||
Db 294 TGTCTCTGCTGATATGCATCATTTGTGATGCTTCTCTGA 332
    |||||

RESULT 39
CHKPLB
LOCUS
  Chicken cardiac phospholamban (plb) mRNA, complete cds.
DEFINITION
  M59039.1 GI:212575
ACCESSION
  M59039.1
VERSION
  keywords
SOURCE
  Gallus gallus (chicken)
  Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  (bases 1 to 3312)
  Toyofuku,T. and Zak,R.
  Characterization of cDNA and genomic sequences encoding a chicken
  phospholamban
  J. Biol. Chem. 266 (9), 5375-5383 (1991)
  1825996
COMMENT
  Original source text: Chicken (broiler breeders) 7-week old adult
  heart, cDNA to mRNA, clones CPL-16,12,15].
FEATURES
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/db_xref="taxon:9031"
/clone="GPL-1"
/tissue_type="adult"
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/tissue_lib="pEMBL3 chicken genomic"
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ICIVMLL"
polyA_signal 534..539
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polyA_signal 930..935
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polyA_signal 3254..3259
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ORIGIN

Query Match 68.8%; Score 109.4; DB 5; Length 3423;
Best Local Similarity 80.5%; Pred. No. 9.5e-19;
Matches 128; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGCCTCAACATTGAATG 60
Db 209 ATGAGAAAGTCCAAATACCAATACCCGCTCTGCTGAGGAGAGCCTCAACTCTTGAGGTC 268

QY 61 CCTCAAGACAGCTCAAGCTCAAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 269 AACCACAAGCAGCCAAAGGCTCCAGAGCTCTTGTGAATTTCTGCTGATCTTAATT 328

QY 121 TGTCTTGTGATCTGATCATCTGATGCTTCTCTGA 159
Db 329 TGCCTCTTGTGATCTGATCATCTTGTGATGCTCTCTGA 367

RESULT 41
ARI21629 AR121629 315 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 26 from patent US 6160088.
DEFINITION

ACCESSION AR121629
VERSION AR121629.1 GI:14105205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 315)
AUTHORS Rothman,J.E., Mayhew,M. and Hoe,M.H.
TITLE KOEL receptor inhibitors
JOURNAL Patent: US 6160088-A 26 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..315
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 52.2%; Score 83; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAAGCTACAGAATCTATTATCAATTTCTGTCATCTTATATGCTCTGCTGA 133
Db 98 GTCAAAAGCTACAGAATCTATTATCAATTTCTGTCATCTTATATGCTCTGCTGA 157

QY 134 TCTGTATCATCTGATGCTTCTC 156
Db 158 TCTGTATCATCTGATGCTTCTC 180

RESULT 42
CR926459/c 132837 bp DNA linear VPT 26-FEB-2005
LOCUS Zebrafish DNA sequence from clone CH211-260022 in linkage group 20,
DEFINITION complete sequence.
ACCESSION CR926459
VERSION CR926459.7 GI:60302549
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 132837)
AUTHORS Henderson,C.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 26, 2005 this sequence version replaced gi:60098210.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhihong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-260022 is from a CHORI-211 BAC library

VECTOR: PTARBAC2.1.

FEATURES

source

1. .132837
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone_lib="CH211-260022"
/clone_lib="CHORI-211"

ORIGIN

Query Match 46.7%; Score 74.2; DB 5; Length 132837;
Best Local Similarity 66.7%; Pred. No. 1.3e-09;
Matches 106; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGCCTCAACCATTTGAATG 60
|||||
DB 6222 ATGGAGAGGTGCGACATGACACGGCGGCCATTGCGGGCGGTCACCATGGAGGTT 6163
|||||
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 120
|||||
DB 6162 CCCCAACAGGCCAAGCAGACATGACGAGGAGCTCTTGTCACTTCTGCTCATCTCATC 6103
|||||
QY 121 TGTCTCTTGTCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 159
|||||
DB 6102 TGCCTGCTGCTCATCTACATCATTTGTTGCTTAATGTGA 6064
|||||

RESULT 43

BX537355

LOCUS

DEFINITION Zebrafish DNA sequence from clone DKEY-18H6 in linkage group 20, complete sequence.

ACCESSION BX537355

VERSION BX537355.13

KEYWORDS HTG.

SOURCE

ORGANISM

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
Lovell, J.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (22-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 23, 2004 this sequence version replaced gi:41060381.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zf1sh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL, SW, SWISSPROT, Tr, TREMBL, Wp, WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhihong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-18H6 is from a Zebrafish BAC library

VECTOR: pIndigobac-5.

Location/Qualifiers
1. .133901

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-18H6"
/clone_lib="DanioKey"

ORIGIN

Query Match 46.7%; Score 74.2; DB 5; Length 133901;
Best Local Similarity 66.7%; Pred. No. 1.3e-09;
Matches 106; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGCCTCAACCATTTGAATG 60
|||||
DB 127680 ATGGAGAGGTGCGACATGACACGGCGGCCATTGCGGGCGGTCACCATGGAGGTT 127739
|||||
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 120
|||||
DB 127740 CCCCAACAGGCCAAGCAGACATGACGAGGAGCTCTTGTCACTTCTGCTCATCTCATC 127799
|||||
QY 121 TGTCTCTTGTCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 159
|||||
DB 127800 TGCCTGCTGCTCATCTACATCATTTGTTGCTTAATGTGA 127838
|||||

RESULT 44

BX276081

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (20-MAY-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 20, 2004 this sequence version replaced gi:46194142.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zf1sh-help@sanger.ac.uk

Submitted (20-MAY-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 20, 2004 this sequence version replaced gi:46194142.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zf1sh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; ENBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency where the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/projects/D_rerio/fishmaek.shtml CH211-270G19 is from a CHORI-211 BAC library

VECTOR: pTARBAC2.1.

Location/Qualifiers

1. .130240

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="CH211-270G19"

/clone_lib="CHORI-211"

FEATURES

source

Query Match 44.7%; Score 71; DB 5; Length 130240;

Best Local Similarity 65.4%; Pred. No. 9.3e-09;

Matches 104; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCAATACCTCACTCGTCAGCTATAGAGAGCCCTCAACATTTGAATG 60

DB 92335 ATGGAGCGGGTGCAGCATATGACGCGCTTCGCGATCCGGAGAGCATCCACATCGAGGTG 92394

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGCTCTCATCTTAATA 120

DB 92395 AACCCGAGACCAACGACCTACAGGATCTCATCATCAACTTCTCCCTCATCTTAATC 92454

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159

DB 92455 TGCTGTCTGTCTATCATCATCATGCTCTTGTCTATGTGA 92493

RESULT 45

AC013809/c

LOCUS AC013809 179556 bp DNA linear HTG 13-JUL-2000

DEFINITION Homo sapiens clone RP11-21C18, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC013809

VERSION AC013809.4 GI:9123984

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179556)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-21C18

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179556)

AUTHORS

TITLE

JOURNAL

COMMENT

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Deaellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:7107985.

All repeats were identified using RepeatMasker:

Smt, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3976

Center clone name: 21_C_18

* NOTE: This record contains 191 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1

* 780: contig of 780 bp in length

* 781

* 880: gap of 100 bp

* 881

* 1631: contig of 751 bp in length

* 1632

* 1731: gap of 100 bp

* 1732

* 2490: contig of 759 bp in length

* 2491

* 2590: gap of 100 bp

* 2591

* 3363: contig of 773 bp in length

* 3364

* 3463: gap of 100 bp

* 3464

* 4235: contig of 772 bp in length

* 4236

* 4335: gap of 100 bp

* 4336

* 5117: contig of 782 bp in length

* 5118

* 5217: gap of 100 bp

* 5218

* 6006: contig of 789 bp in length

* 6007

* 6106: gap of 100 bp

* 6107

* 6869: contig of 763 bp in length

* 6870

* 6970: gap of 100 bp

* 6971

* 7733: contig of 764 bp in length

* 7734

* 7833: gap of 100 bp

* 7834

* 8607: contig of 774 bp in length

* 8608

* 8707: gap of 100 bp

* 8708

* 8709: contig of 772 bp in length

* 8710

* 9480: gap of 100 bp

* 9481

* 9579: contig of 765 bp in length

* 9580

* 10344: gap of 100 bp

* 10345

* 10444: gap of 100 bp

* 10445

* 11212: contig of 768 bp in length

* 11213

* 11312: gap of 100 bp

* 11313

* 12066: contig of 754 bp in length

* 12067

* 12166: gap of 100 bp

* 12167

* 12972: contig of 806 bp in length

* 12973

* 13072: gap of 100 bp

* 13073

* 13842: contig of 770 bp in length

* 13843

* 13942: gap of 100 bp

* 13943 14708: contig of 766 bp in length
* 14709 14808: gap of 100 bp
* 14809 15579: contig of 771 bp in length
* 15580 15679: gap of 100 bp
* 15680 16450: contig of 771 bp in length
* 16451 16550: gap of 100 bp
* 16551 17324: contig of 774 bp in length
* 17325 17424: gap of 100 bp
* 17425 18199: contig of 775 bp in length
* 18200 18299: gap of 100 bp
* 18300 19041: contig of 742 bp in length
* 19042 19141: gap of 100 bp
* 19142 19940: contig of 799 bp in length
* 19941 20040: gap of 100 bp
* 20041 20792: contig of 752 bp in length
* 20793 20892: gap of 100 bp
* 20893 21652: contig of 760 bp in length
* 21653 21752: gap of 100 bp
* 21753 22531: contig of 779 bp in length
* 22532 22631: gap of 100 bp
* 22632 23404: contig of 773 bp in length
* 23405 23504: gap of 100 bp
* 24284 24383: gap of 100 bp
* 24384 25152: contig of 769 bp in length
* 25153 25252: gap of 100 bp
* 25253 26020: contig of 768 bp in length
* 26021 26120: gap of 100 bp
* 26121 26894: contig of 774 bp in length
* 26895 27757: contig of 763 bp in length
* 27758 28638: contig of 781 bp in length
* 28639 29512: contig of 774 bp in length
* 29513 29612: gap of 100 bp
* 29613 30394: contig of 782 bp in length
* 30395 30494: gap of 100 bp
* 30495 31270: contig of 776 bp in length
* 31271 31370: gap of 100 bp
* 31371 32140: contig of 770 bp in length
* 32141 32240: gap of 100 bp
* 32241 33008: contig of 768 bp in length
* 33009 33108: gap of 100 bp
* 33109 33891: contig of 783 bp in length
* 33892 33991: gap of 100 bp
* 33992 34774: contig of 783 bp in length
* 34775 34874: gap of 100 bp
* 34875 35638: contig of 764 bp in length
* 35639 35738: gap of 100 bp
* 35739 36511: contig of 773 bp in length
* 36512 37381: contig of 770 bp in length
* 37382 37481: gap of 100 bp
* 37482 38270: contig of 789 bp in length
* 38271 38370: gap of 100 bp
* 38371 39151: contig of 781 bp in length
* 39152 39251: gap of 100 bp
* 39252 40022: contig of 771 bp in length
* 40023 40122: gap of 100 bp
* 40123 40894: contig of 772 bp in length
* 40895 40994: gap of 100 bp
* 40995 41765: contig of 771 bp in length
* 41766 41865: gap of 100 bp
* 41866 42619: contig of 754 bp in length
* 42620 42719: gap of 100 bp
* 42720 43503: contig of 784 bp in length
* 43504 43603: gap of 100 bp
* 43604 44367: contig of 764 bp in length
* 44368 44467: gap of 100 bp
* 44468 45241: contig of 774 bp in length
* 45242 45341: gap of 100 bp
* 45342 46113: contig of 772 bp in length

* 46114 46213: gap of 100 bp
* 46214 49882: contig of 769 bp in length
* 49883 49882: gap of 100 bp
* 47083 47847: contig of 765 bp in length
* 47848 47947: gap of 100 bp
* 47948 48720: contig of 773 bp in length
* 48721 48820: gap of 100 bp
* 48821 49593: contig of 773 bp in length
* 49594 49693: gap of 100 bp
* 49694 50493: contig of 800 bp in length
* 50494 50593: gap of 100 bp
* 50594 51359: contig of 766 bp in length
* 51360 51459: gap of 100 bp
* 51460 52244: contig of 785 bp in length
* 52245 52344: gap of 100 bp
* 52345 53132: contig of 788 bp in length
* 53133 53232: gap of 100 bp
* 53233 53993: contig of 761 bp in length
* 53994 54093: gap of 100 bp
* 54094 54863: contig of 770 bp in length
* 54864 54963: gap of 100 bp
* 54964 55732: contig of 769 bp in length
* 55733 55832: gap of 100 bp
* 55833 56605: contig of 773 bp in length
* 56606 56705: gap of 100 bp
* 56706 57460: contig of 755 bp in length
* 57461 57560: gap of 100 bp
* 57561 58365: contig of 805 bp in length
* 58366 58465: gap of 100 bp
* 58466 59226: contig of 761 bp in length
* 59227 59326: gap of 100 bp
* 59327 60099: contig of 773 bp in length
* 60099 60199: gap of 100 bp
* 60199 60958: contig of 759 bp in length
* 60959 61058: gap of 100 bp
* 61059 61857: contig of 799 bp in length
* 61858 61957: gap of 100 bp
* 61958 62741: contig of 784 bp in length
* 62742 62841: gap of 100 bp

Query Match 26.0%; Score 41.4; DB 14; Length 179556;
Best Local Similarity 97.7%; Pred. No. 0.66;
Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCCTCGTCTCAGCTATAGAGAG 43
Db 134352 ATGGAGAAAGTCCAAATACCTCCTCGTCTCAGCTATAGAGAGG 134310

RESULT 46
AC025771

LOCUS AC025771 134286 bp DNA linear PRI 03-OCT-2001
DEFINITION Homo sapiens chromosome 5 clone CTD-2203L19, complete sequence.

ACCESSION AC025771

VERSION AC025771.6 GI:15887314

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 134286)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 134286)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (14-MAR-2000) Production Sequencing Facility, DOE Joint

AUTHORS Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 134286)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 134286)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Oct 3, 2001 this sequence version replaced gi:10312259.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;

Estimated Total Number of Errors is 0.6.

Location/Qualifiers

1..134286

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTD-2203L19"

ORIGIN

Query Match 23.1%; Score 36.8; DB 8; Length 134286;

Best Local Similarity 58.0%; Pred. No. 11;

Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 46 TCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTC 105

Db 40650 TCAACCTTTGATCGATTCTACATATAAGTGAACCGTACAGAAATTTTCATCTGTTTC 40709

QY 106 TGTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTATGCTTCTCT 157

Db 40710 TGGCTTATTTCTACGTAGCATATAATAGGCTCTCTAAATTCATCTGTTTTT 40761

RESULT 47

AC024589 170272 bp DNA linear PRI 15-AUG-2001

LOCUS Homo sapiens chromosome 5 clone RP11-42L13, complete sequence.

DEFINITION AC024589

ACCESSION AC024589.5 GI:15187245

VERSION HTG.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Aug 15, 2001 this sequence version replaced gi:13173623.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.8% of Sequence;

Estimated Total Number of Errors is 0.2.

Location/Qualifiers

1..170272

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-42L13"

ORIGIN

Query Match 23.1%; Score 36.8; DB 8; Length 170272;

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Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db 9253 TCAACCTTTGATCGATTCTACATATAAGTGAACCGTACAGAAATTTTCATCTGTTTC 9312

QY 106 TGTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTATGCTTCTCT 157

Db 9313 TGGCTTATTTCTACGTAGCATATAATAGGCTCTCTAAATTCATCTGTTTTT 9364

RESULT 48

AL590653 116103 bp DNA linear PRI 18-MAY-2005

LOCUS Human DNA sequence from clone RP11-142B3 on chromosome 1 Contains part of the gene for melanoma antigen recognized by T cells 2

DEFINITION Protein (MART2), complete sequence.

ACCESSION AL590653

VERSION GI:17384115

KEYWORDS HTG; MART2; melanoma antigen; T cells 2 protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 116103)

AUTHORS Hartison,E.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

COMMENT On Dec 5, 2001 this sequence version replaced gi:17127779.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chrl

RP11-142B3 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers

1..116103

/organism="Homo sapiens"

FEATURES

source


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ORIGIN

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RESULT 49
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LOCUS Ornithorhynchus anatinus clone OA_Bb-338A1, WORKING DRAFT SEQUENCE,
DEFINITION 7 ordered pieces.
AC158428
AC158428.2 GI:70778563
VERSION HTG: HTGS_PHASE2: HTGS_DRAFT.
KEYWORDS Ornithorhynchus anatinus
SOURCE Ornithorhynchus anatinus
ORGANISM Ornithorhynchus anatinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
1 (bases 1 to 136485)
REFERENCE
AUTHORS Antonellis,A., Ayele,K., Bags,D., Benjamin,B., Bera,J.,
Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G.,
Coleman,H., Engle,J., Fuxsenko,T., Gestole,M., Greene,A., Guan,X.,
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Hunter,G., Hurlb,B., Idol,J.R., Kwong,P., Laric,P., Larson,S.,
Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masello,C., Maekeri,B., McDowell,J., Mojidi,H.A.,
Mullikin,J.C., Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A.,
Puri,O., Reddx-Dugue,N., Sante,A., Schandler,K., Schueler,M.G.,
Sison,C., Stantropop,S., Stephen,E., Taye,A., Thomas,J.W.,
Thomas,P.J., Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D.,
Withers,T.R., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 136485)
Green,E.D.
Direct Submission
Submitted (16-MAR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 136485)
Green,E.D.
Direct Submission
Submitted (13-JUL-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Jul 13, 2005 this sequence version replaced gi:61326072.

----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: jbm
Center clone name: 338A01

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is generally based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out

gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 134683 bases at least Q40
Consensus quality: 135292 bases at least Q30
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Insert size: 139000; agarose-fp
Insert size: 135885; sum-of-contigs
Quality coverage: 9.53x in Q20 bases; agarose-fp
Quality coverage: 9.75x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 13130: contig of 13130 bp in length
* 13131 13230: gap of unknown length
* 13231 25045: contig of 11815 bp in length
* 25046 25145: gap of unknown length
* 25146 64059: contig of 38914 bp in length
* 64060 64159: gap of unknown length
* 64160 70711: contig of 6552 bp in length
* 70712 70811: gap of unknown length
* 70812 76877: contig of 6066 bp in length
* 76878 76977: contig of 31977 bp in length
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 20:37:40 ; Search time 479 Seconds
(without alignments)

2212.288 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atggagaaagccaataacct.....tcacgtgatgcttctctga 159

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	159	100.0	480	3	Aac06724 Human sec
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4	159	100.0	1635	6	Ab161825 Colon ade
5	159	100.0	1635	12	Adn04087 Antipsori
6	159	100.0	1712	12	Adp21384 Gene PLN
7	159	100.0	1712	14	Aea81478 Human Pho
8	158	99.4	380	9	Ach16738 Human adu
9	158	99.4	418	9	Ach18023 Human adu
10	157.4	99.0	394	9	Ach17005 Human adu
11	147.8	93.0	487	9	Ach18165 Human adu
12	147.8	93.0	492	9	Ach30165 Human tes
13	144.6	90.9	407	9	Ach16630 Human adu
14	143	89.9	159	3	Aac64967 Pig phosph
15	127.6	80.3	306	6	Abn22344 Human ORF
16	123.8	77.9	701	10	AdB53082 Primary r
17	83	52.2	312	3	Aaz50498 KDEL rece
18	46	28.9	108	13	AdA18082 Human/mou
19	46	28.9	108	13	AdS18083 Human/mou

C	20	46	28.9	135	13	ADSI18085
C	21	46	28.9	135	13	ADSI18084
C	22	34.8	21.9	101169	12	ADQ97584
C	23	34.6	21.8	2043	2	AAX59526
C	24	34.6	21.8	2071	2	AAV46494
C	25	33.4	21.0	37973	6	ABL34196
C	26	33.2	20.9	80268	13	ABD32951
C	27	32.6	20.5	170279	13	ABD32686
C	28	32.2	20.3	3713	2	AAQ64111
C	29	32.2	20.3	3713	2	AAT95050
C	30	32.2	20.3	3713	2	AAT68435
C	31	32.2	20.3	3713	2	AAV83926
C	32	32.2	20.3	3713	2	AAZ09159
C	33	32.2	20.3	127432	12	ADQ43653
C	34	32	20.1	1590	12	ADN73394
C	35	31.8	20.0	1421	2	AAV74594
C	36	31.8	20.0	6025	14	ADW94142
C	37	31.4	19.7	873	5	AAS69551
C	38	31.4	19.7	873	5	AAS69244
C	39	31.4	19.7	873	5	AAS75469
C	40	31.4	19.7	2000	11	ACL38668
C	41	31.4	19.7	3505	4	ABL19916
C	42	31.4	19.7	5875	6	ABL32288
C	43	31.2	19.6	84073	11	ACN44322
C	44	31	19.5	1269	13	ADR60694
C	45	31	19.5	6182	6	ABL34015
C	46	31	19.5	271990	10	ADD25213
C	47	31	19.5	271990	12	ADN61228
C	48	30.8	19.4	437	13	ADR61212
C	49	30.8	19.4	2090	2	AAQ62612
C	50	30.8	19.4	3060	14	ADY95063
C	51	30.8	19.4	3060	14	ADZ26757
C	52	30.8	19.4	8573	6	ABS98184
C	53	30.8	19.4	10200	6	AAD41243
C	54	30.8	19.4	177380	8	ACF62751
C	55	30.8	19.4	177380	8	ADB20870
C	56	30.8	19.4	177380	10	ADB87959
C	57	30.8	19.4	177380	10	ADB96942
C	58	30.8	19.4	177380	10	ADB92133
C	59	30.6	19.2	349	8	ABX36263
C	60	30.6	19.2	496	9	ACH37982
C	61	30.6	19.2	551	6	ABL83073
C	62	30.6	19.2	930	4	AAS30994
C	63	30.6	19.2	1132	4	AAS34823
C	64	30.6	19.2	1132	10	ADC45981
C	65	30.6	19.2	1434	4	AAI59427
C	66	30.6	19.2	1592	4	AAH14974
C	67	30.6	19.2	1973	5	ADL61951
C	68	30.6	19.2	2571	4	AAI61213
C	69	30.6	19.2	2615	5	AAD02597
C	70	30.6	19.2	2617	13	ADR66787
C	71	30.6	19.2	2617	13	ADR65884
C	72	30.6	19.2	89873	13	ABD32846
C	73	30.6	19.2	95109	6	ABQ99654
C	74	30.4	19.1	371	4	AAH29390
C	75	30.4	19.1	1209	10	ADF73039
C	76	30.2	19.0	277	6	ABL72882
C	77	30.2	19.0	612	5	ABV06511
C	78	30.2	19.0	18678	4	AAK91271
C	79	30.2	19.0	18678	4	AAS32889
C	80	30.2	19.0	25002	6	ABQ74278
C	81	30.2	19.0	25002	12	ADL27983
C	82	30.2	19.0	34203	11	ACN45106
C	83	30.2	19.0	110000	10	ACF42745_2
C	84	30.2	19.0	110000	13	ABD32966_04
C	85	30.2	19.0	110000	13	ABD32966_05
C	86	30.2	19.0	198073	11	ACN44302
C	87	30	18.9	475	3	AAA43951
C	88	30	18.9	859	2	ACF62810
C	89	30	18.9	2986	8	ACF62810
C	90	30	18.9	3486	8	ABZ10140
C	91	30	18.9	3486	10	ABZ10140
C	92	30	18.9	3486	10	ABZ10140

c 93 30 18.9 3486 13 ADS89540 Oligonuc1
94 30 18.9 142519 10 AAD54634 Human chr
95 30 18.9 243390 13 ABD33366 Human can
96 30 18.9 243394 14 ADZ13446 Human can
97 29.8 18.7 413 6 ABN76328 Human ORF
98 29.8 18.7 711 6 ABS76838 Frog embr
99 29.8 18.7 765 13 ADR99954 Immune Re
100 29.8 18.7 972 14 ADV42443 Human psy

ALIGNMENTS

RESULT 1
ADR97285
ID ADR97285 standard; DNA; 159 BP.
XX
AC ADR97285;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human phospholamban polymorphism fragment DNA.
XX
KW ds; human; phospholamban; polymorphism; cardiovascular disease.
XX
OS Homo sapiens.
XX
PN US2004191802-A1.
XX
PD 30-SEP-2004.
XX
PF 22-OCT-2003; 2003US-00691412.
XX
PR 22-OCT-2002; 2002US-0420295P.
XX
PA (KRAN/) KRANIAS E G.
PA (HAGH/) HAGHIGHI K.
XX
PI Kranias EG, Haghighi K;
XX
DR WPI; 2004-689841/67.
XX
PT Phospholamban polymorphism assessment in individual, for determining risk
PT for developing cardiovascular disease, by comparing analysis of the
PT nucleotide fragment with a predetermined phospholamban nucleotide
PT fragment sequence.
XX
PS Claim 15; SEQ ID NO 1; 15pp; English.
XX
CC The invention relates to a method of phospholamban polymorphism
CC assessment in an individual which comprises comparing the analysis of the
CC nucleotide fragment with a predetermined phospholamban nucleotide
CC fragment sequence to determine whether the individual carries a
CC phospholamban polymorphism. The methods and phospholamban polymorphism
CC fragment are useful for determining if an individual is at risk for
CC developing a cardiovascular disease. The present sequence represents the
CC human phospholamban polymorphism fragment DNA.
XX
SQ Sequence 159 BP; 48 A; 39 C; 24 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 13; Length 159;
Best Local Similarity 100.0%; Pred. No. 9e-39;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTAGCTATAAGAGAGCCTCAACCAATTGAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTAGCTATAAGAGAGCCTCAACCAATTGAATG 60
QY 61 CCTCAACAGCACGTCGCTCAAGAGCTACAGAACTTATTTATCAATTTCTCTCATCTTAATA 120
DB 61 CCTCAACAGCACGTCGCTCAAGAGCTACAGAACTTATTTATCAATTTCTCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 159

DB 121 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 159

RESULT 2
AAC06724
ID AAC06724 standard; cDNA; 480 BP.
XX
AC AAC06724;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 10799.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 10799; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 480 BP; 149 A; 120 C; 76 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTAGCTATAAGAGAGCCTCAACCAATTGAATG 60
DB 196 ATGGAGAAAGTCCAAATACCTCAGCTCGCTAGCTATAAGAGAGCCTCAACCAATTGAATG 255
QY 61 CCTCAACAGCACGTCGCTCAAGAGCTACAGAACTTATTTATCAATTTCTCTCATCTTAATA 120
DB 256 CCTCAACAGCACGTCGCTCAAGAGCTACAGAACTTATTTATCAATTTCTCTCATCTTAATA 315
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 159
DB 316 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 354

RESULT 3
ACH16833
ID ACH16833 standard; cDNA; 525 BP.
XX
XX ACH16833;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human adult heart cDNA #1147.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 4045; 44bp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 525 BP; 150 A; 153 C; 80 G; 140 T; 0 U; 2 Other;
XX
XX Query Match 100.0%; Score 159; DB 9; Length 525;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-38;
XX Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGAGAAAGTCAATACCTACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAATG 60
XX
XX 310 ATGGAGAAAGTCAATACCTACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAATG 369
XX
XX 61 CCTCAACAGCAGCTCAAGAGTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
XX
XX 370 CCTCAACAGCAGCTCAAGAGTACAGATCTATTATCAATTTCTGCTCATCTTAATA 429
XX
XX 121 TGTCTCTTGTGATCTGATCATCATGTCGTCTCTCTGA 159

Db 430 TGTCTCTTGTGATCTGATCATCATGTCGTCTCTCTGA 468
RESULT 4
ABL61825
ID ABL61825 standard; DNA; 1635 BP.
XX
XX ABL61825;
XX
XX 15-MAY-2002 (first entry)
XX
XX Colon adenocarcinoma related gene sequence SEQ ID NO:162.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; Gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
XX 05-JUN-2000; 2000US-0209531P.
XX 18-SEP-2000; 2000US-0233133P.
XX 18-SEP-2000; 2000US-0233617P.
XX 20-SEP-2000; 2000US-0234009P.
XX 20-SEP-2000; 2000US-0234034P.
XX 20-SEP-2000; 2000US-0234052P.
XX 22-SEP-2000; 2000US-0234509P.
XX 22-SEP-2000; 2000US-0234567P.
XX 25-SEP-2000; 2000US-0234923P.
XX 25-SEP-2000; 2000US-0234924P.
XX 25-SEP-2000; 2000US-0235077P.
XX 25-SEP-2000; 2000US-0235082P.
XX 25-SEP-2000; 2000US-0235134P.
XX 26-SEP-2000; 2000US-0235280P.
XX 26-SEP-2000; 2000US-0235637P.
XX 26-SEP-2000; 2000US-0235638P.
XX 27-SEP-2000; 2000US-0235711P.
XX 27-SEP-2000; 2000US-0235720P.
XX 27-SEP-2000; 2000US-0235840P.
XX 27-SEP-2000; 2000US-0235863P.
XX 28-SEP-2000; 2000US-0236028P.
XX 28-SEP-2000; 2000US-0236032P.
XX 28-SEP-2000; 2000US-0236033P.
XX 28-SEP-2000; 2000US-0236034P.
XX 28-SEP-2000; 2000US-0236109P.
XX 28-SEP-2000; 2000US-0236111P.
XX 29-SEP-2000; 2000US-0236842P.
XX 29-SEP-2000; 2000US-0236891P.
XX 02-OCT-2000; 2000US-0237172P.
XX 02-OCT-2000; 2000US-0237173P.
XX 02-OCT-2000; 2000US-0237278P.
XX 02-OCT-2000; 2000US-0237294P.
XX 02-OCT-2000; 2000US-0237295P.
XX 02-OCT-2000; 2000US-0237316P.
XX 03-OCT-2000; 2000US-0237425P.
XX 03-OCT-2000; 2000US-0237598P.
XX 03-OCT-2000; 2000US-0237604P.
XX 03-OCT-2000; 2000US-0237606P.
XX 03-OCT-2000; 2000US-0237608P.
XX 01-NOV-2000; 2000US-0244867P.
XX 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI

PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 162; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in AB61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
XX tumour
XX Sequence 1635 BP; 567 A; 309 C; 231 G; 528 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 6; Length 1635;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGAGCCCTCAACCAATTGAAATG 60
DB 182 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGAGCCCTCAACCAATTGAAATG 241
QY 61 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
DB 242 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340
RESULT 5
ADN04087
XX ADN04087 standard; cDNA; 1635 BP.
XX
XX AC ADN04087;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Antipsoriatic cDNA sequence #243.
XX
XX KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX OS Homo sapiens.
XX
XX FN WO2004028479-A2.
XX
XX PD 08-APR-2004.
XX
XX PF 25-SEP-2003; 2003WO-US030907.
XX
XX PR 25-SEP-2002; 2002US-0414006P.
XX
XX PA (GETH) GENENTECH INC.
XX
XX FI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-305105/28.
DR P-PSDB; ADN04088.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 1; SEQ ID NO 481; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
XX SQ Sequence 1635 BP; 567 A; 309 C; 231 G; 528 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 12; Length 1635;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGAGCCCTCAACCAATTGAAATG 60
DB 182 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGAGCCCTCAACCAATTGAAATG 241
QY 61 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
DB 242 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340
RESULT 6
ADP21384
ID ADP21384 standard; DNA; 1712 BP.
XX
XX AC ADP21384;
XX
XX DT 09-SEP-2004 (first entry)
XX
XX DE Gene PLN for screening for cardiac therapeutic preparation.
XX
XX KW ds; cardiant; gene therapy; cardiac therapeutic preparation;
KW beta-adrenergic receptor antagonist; endothelial receptor antagonist;
KW calcium channel antagonist; phosphodiesterase inhibitor;
KW angiotensin converting enzyme inhibitor; heart failure.
XX
XX OS Homo sapiens.
XX
XX PN WO2004050894-A2.
XX
XX PD 17-JUN-2004.
XX
XX PF 26-NOV-2003; 2003WO-US037927.
XX
XX PR 27-NOV-2002; 2002US-0429379P.
XX
XX PR 31-DEC-2002; 2002US-0437051P.
XX
XX PR 31-DEC-2002; 2002US-0437102P.
XX
XX PA (ARTE-) ARTESIAN THERAPEUTICS INC.
XX
XX FI Bednarik DP;
XX
XX DR WPI; 2004-450738/42.
XX
XX Screening potential therapeutic compounds for cardiac therapeutic
PT preparations, useful for treating heart failure in a subject, comprises
PT contacting a sample of cell or tissue with a compound and detecting gene
PT expression level.
XX

PS Claim 10; SEQ ID NO 58; 152pp; English.
 XX
 CC The invention relates to a method of screening potential therapeutic
 CC compounds for cardiac therapeutic preparations by contacting a sample
 CC comprising a cell or tissue with a potential therapeutic compound and
 CC detecting a level of expression of a gene that codes for a product
 CC encoded by a nucleic acid selected from 98 sequences given in the
 CC specification and its conservative variants, comparing the level of the
 CC expression of the gene to the level of expression of the gene in the
 CC absence of the compound, and identifying a potential therapeutic compound
 CC for use as a cardiac therapeutic preparation if the potential therapeutic
 CC compound affects the level of expression of the gene. The pharmaceutical
 CC composition or active agents (i.e., beta-adrenergic receptor antagonist,
 CC endothelial receptor antagonist, calcium channel antagonist,
 CC phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)
 CC is useful for treating heart failure in a subject. This sequence
 CC represents one of the genes whose expression may be altered by the
 CC compounds detected by the screen of the invention.
 XX
 SQ Sequence 1712 BP; 618 A; 313 C; 240 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 12; Length 1712;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
 DB 182 ATGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTCTCTGA 340

RESULT 8
 ACH16738
 ID ACH16738 standard; cDNA; 380 BP.
 AC ACH16738;
 DT 13-OCT-2003 (first entry)
 XX Human adult heart cDNA #1052.
 DE Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS US2003073623-A1.
 PN 17-APR-2003.
 PD 30-JUL-2001; 2001US-00918995.
 PF 30-JUL-2001; 2001US-00918995.
 PR (DRMA/) DRMANAC R T.
 XX (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

PS Claim 10; SEQ ID NO 58; 152pp; English.
 XX
 CC The invention relates to a method of screening potential therapeutic
 CC compounds for cardiac therapeutic preparations by contacting a sample
 CC comprising a cell or tissue with a potential therapeutic compound and
 CC detecting a level of expression of a gene that codes for a product
 CC encoded by a nucleic acid selected from 98 sequences given in the
 CC specification and its conservative variants, comparing the level of the
 CC expression of the gene to the level of expression of the gene in the
 CC absence of the compound, and identifying a potential therapeutic compound
 CC for use as a cardiac therapeutic preparation if the potential therapeutic
 CC compound affects the level of expression of the gene. The pharmaceutical
 CC composition or active agents (i.e., beta-adrenergic receptor antagonist,
 CC endothelial receptor antagonist, calcium channel antagonist,
 CC phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)
 CC is useful for treating heart failure in a subject. This sequence
 CC represents one of the genes whose expression may be altered by the
 CC compounds detected by the screen of the invention.
 XX
 SQ Sequence 1712 BP; 618 A; 313 C; 240 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 12; Length 1712;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
 DB 182 ATGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTATCATCGTATCTCTCTGA 340

RESULT 7
 AEA81478
 ID AEA81478 standard; cDNA; 1712 BP.
 AC AEA81478;
 DT 08-SEP-2005 (first entry)
 XX Human Phospholamban cDNA.
 DE Anorectic; obesity; cachexia; anabolic; genetic marker; skeletal muscle;
 KW ss; gene; drug screening.
 XX Homo sapiens.
 OS EP1548131-A2.
 PN 29-JUN-2005.
 PD 15-DEC-2004; 2004EP-00029642.
 PF 22-DEC-2003; 2003EP-00104899.
 PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (OSTE/) OSTENSON C.
 XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
 PI WPI: 2005-460899/47.
 DR P-PSDB; AEA81486.
 XX Screening compounds that reduce and/or prevent obesity, and/or treat
 PT cachexia, by contacting a cell expressing down-regulated or up-regulated
 PT genes in skeletal muscle in obesity.

XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 4217; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 394 BP; 115 A; 107 C; 58 G; 113 T; 0 U; 1 Other;
SQ
Query Match 99.0%; Score 157.4; DB 9; Length 394;
Best Local Similarity 99.4%; Pred. No. 3.7e-39;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAAATG 60
Db 182 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAAATG 241
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 242 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340
RESULT 11
ACH18165
ID ACH18165 standard; cDNA; 487 BP.
XX ACH18165;
XX
XX 13-OCT-2003 (first entry)
DE Human adult heart cDNA #2479.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS US2003073623-A1.
PD 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 5377; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 487 BP; 135 A; 140 C; 87 G; 122 T; 0 U; 3 Other;
SQ
Query Match 93.0%; Score 147.8; DB 9; Length 487;
Best Local Similarity 95.6%; Pred. No. 3.4e-35;
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAAATG 60
Db 252 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAAATG 311
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 312 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 371
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 372 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 410
RESULT 12
ACH30165
ID ACH30165 standard; cDNA; 492 BP.
XX ACH30165;
XX
XX 13-OCT-2003 (first entry)
DE Human testis cDNA #551.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995.

(DRMA/) DRMANAC R T.

(LABA/) LABAT I.

(STAC/) STACHE-CRAIN B.

(DICK/) DICKSON M C.

(JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 3842; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 407 BP; 116 A; 102 C; 76 G; 113 T; 0 U; 0 Other;

Query Match 90.9%; Score 144.6; DB 9; Length 407;

Best Local Similarity 94.3%; Pred. No. 3.1e-34;

Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCTCAACCAATTGAATG 60

Db 182 ATGGAGAAAGTCAATAATACCTCAGCTATAGAGAGAGCTCAACCAATTGAATG 241

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 120

Db 242 CCTCAGCAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 301

QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 302 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 340

RESULT 14

AAC64967

ID AAC64967 standard; cDNA; 159 BP.

XX AAC64967;

XX

us-10-691-412-1.rng

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995.

(DRMA/) DRMANAC R T.

(LABA/) LABAT I.

(STAC/) STACHE-CRAIN B.

(DICK/) DICKSON M C.

(JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 17377; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 492 BP; 141 A; 136 C; 88 G; 125 T; 0 U; 2 Other;

Query Match 93.0%; Score 147.8; DB 9; Length 492;

Best Local Similarity 95.6%; Pred. No. 3.4e-35;

Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCTCAACCAATTGAATG 60

Db 278 ATGGAGAAAGGCCAATAATACCTCAGCTATAGAGAGAGCTCAACCAATTGAATG 337

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 120

Db 338 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 397

QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 398 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 436

RESULT 13

ACH16630

ID ACH16630 standard; cDNA; 407 BP.

XX ACH16630;

XX ACH16630;

DT 13-OCT-2003 (first entry)

XX Human adult heart cDNA #944.

XX

Dt	09-FEB-2001 (first entry)
DE	Pig phospholamban cDNA.
KW	Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;
KW	cardiac hypertrophy; heart failure; hypertension; Darier-White disease;
KW	Brody's disease; diabetes; ss.
XX	
OS	Sus scrofa.
XX	
PN	GB2349217-A.
XX	
PD	25-OCT-2000.
XX	
PF	14-APR-2000; 2000GB-00009363.
XX	
PR	15-APR-1999; 99GB-00008670.
PR	15-APR-1999; 99US-0129596P.
PR	01-JUN-1999; 99GB-00012736.
XX	
PA	(DEVG-) DEVGEN NV.
PI	Zwaal R, Groenen J, Bogaert T;
XX	
DR	WPI; 2000-658082/64.
XX	
PT	Identifying modulators of sarco/endoplasmic reticulum calcium ATPase,
PT	useful potentially for treating disorders of calcium homeostasis, e.g.
PT	cardiac hypertrophy.
XX	
PS	Disclosure; Fig 11; 108pp; English.
XX	
CC	The present invention is concerned with methods of using C. elegans to
CC	identify compounds which are capable of up- and down-regulating the
CC	activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This
CC	protein is involved in cell signalling, and elevated levels affect
CC	cellular processes such as contraction, secretion and cell cycling. The
CC	methods can be used to identify compounds for use in the treatment of
CC	some muscle pathologies, cardiac hypertrophy, heart failure,
CC	hypertension, diabetes, Darier-White disease and Brody's disease
XX	
SQ	Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;
	Query Match 89.9%; Score 143; DB 3; Length 159;
	Best Local Similarity 93.7%; Pred. No. 7.2e-34;
	Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 ATGGAGAAATGCCAATACCTCAGTCTCGCTCAGTTATAAGAAGAGCTCAACCATGAATG 60
Db	
	1 ATGGATAAATGCCAATACCTCAGTCTCGCTCAGTTATAAGAAGAGCTCAACCATGAATG 60
Qy	61 CCTCAACAAGCAGCTCAAAGCTACAGAACTATTATTCATTTTGCTCTCTTAATA 120
Db	
	61 CCTCAACAAGCAGCTCAAAGCTACAGAACTATTATTCATTTTGCTCTCTTAATA 120
Qy	121 TGCTCTTGCTGATCTGTATCATCGTAGCTTCTCTGA 159
Db	
	121 TGCTCTTGCTGATTTGGATCATCGTAGCTTCTCTGA 159
RESULT 15	
ID	ABN22344
AB	ABN22344 standard; cDNA; 306 BP.
XX	
AC	ABN22344;
XX	
DT	24-JUN-2002 (first entry)
XX	
DE	Human ORFX polynucleotide sequence SEQ ID NO:13165.
XX	
KW	Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW	hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW	degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX	

KW	cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW	hypertension; hypothyroidism; cholesterol ester storage disease;
KW	immune deficiency; immune disorder; infectious disease;
KW	autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX	myasthenia gravis; gene; ss.
OS	Homo sapiens.
XX	
PN	WO200192523-A2.
XX	
PD	06-DEC-2001.
XX	
PF	29-MAY-2001; 2001WO-US010836.
XX	
PR	30-MAY-2000; 2000US-0206132P.
PR	29-AUG-2000; 2000US-0228716P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach MD;
XX	
DR	WPI; 2002-106308/14.
DR	P-PDSB; ABP06592.
XX	
PT	Novel human polypeptides and polynucleotides useful for diagnosing,
PT	preventing and treating cardiovascular disease, neurodegenerative,
PT	hyperproliferative disorders and autoimmune disorders.
XX	
FS	Disclosure; SEQ ID NO 13165; 1037pp; English.
XX	
CC	The present invention describes substantially purified human proteins
CC	(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC	in the specification)). ABN15762 to ABN27252 encode the human ORFX
CC	proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC	treating or preventing a pathology associated with an ORFX-associated
CC	disorder in humans, and in the manufacture of a medicament for treating a
CC	syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC	sequences can be used in gene therapy. ORFX sequences can be used in the
CC	treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC	psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC	osteoarthritis, neurodegenerative diseases, disorders related to organ
CC	transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC	lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC	storage disease, various immune deficiencies and disorders, infectious
CC	diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC	arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC	disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC	useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC	bone degenerative disorders, or periodontal disease, and for gut
CC	protection or regeneration and treatment of lung or liver fibrosis,
CC	reperfusion injury in various tissues and conditions resulting from
CC	systemic cytokine damage. N.B. The sequence data for this patent did not
CC	form part of the printed specification, but was obtained in electronic
CC	format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 306 BP; 76 A; 84 C; 56 G; 88 T; 0 U; 2 Other;
	Query Match 80.3%; Score 127.6; DB 6; Length 306;
	Best Local Similarity 87.4%; Pred. No. 4.6e-29;
	Matches 139; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy	1 ATGGAGAAAGTCCAATACCTCAGTCTCAGCTATAGAAGAGGCTCAACCATGAATG 60
Db	
	127 ATGGAAAAGTGCAATATCTCACTCGCTCGGCTATCAGGAGGCTCCACTATTGAATG 186
Qy	61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTCATTTTGCTCTCTTAATA 120
Db	
	187 CCTCAGCAGCACGCTCAGAACTCTCAGAACCTATTATTCATTTTGCTCTCTTAATA 120
Qy	121 TGCTCTTGCTGATCTGTATCATCGTAGCTTCTCTGA 159
Db	
	247 TGCTCTTGCTGATCTGTATCATTTGNGATGCTTCTCTGA 285

XX PS Disclosure; Fig 7; 87pp; English.

CC The patent discloses the use of KDEL receptor inhibitor to promote

CC secretion of proteins that are normally retained within the cell such as

CC heat shock proteins by inhibiting KDEL receptor-mediated return of

CC protein complexes to endoplasmic reticulum. This makes the secreted heat

CC shock proteins more accessible to the immune system and improves immune

CC response to a target antigen. The inhibitor protein comprises several

CC subunits where each subunit comprises an oligomerisation domain and has

CC at its carboxy terminus a region which binds to a KDEL receptor. The

CC target antigen may be associated with diseases including neoplasia such

CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and

CC astrocytoma, with defective tumour suppressor genes, oncogenes,

CC infectious diseases, allergy or autoimmune diseases. The present sequence

CC encodes KDEL receptor inhibitor comprising regions encoding a cleavable

CC signal peptide; the oligomerisation domain of human phospholamban (PLB)

CC pentamerisation domain; a camel IgG linker domain and the carboxy-

CC terminal sequence KDEL. The subsequence GDCC is an alteration of rat

CC cartilage oligomeric matrix protein which provides increased stability

CC via disulphide bonds. (Updated on 15-SEP-2003 to standardise OS field)

XX SQ Sequence 312 BP; 80 A; 85 C; 77 G; 70 T; 0 U; 0 Other;

Query Match 52.2%; Score 83; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 GTCAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTATATGCTCTTGTGCTGA 133
Db 95 GTCAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTATATGCTCTTGTGCTGA 154

Qy 134 TCTGTATCATGCTGATGCTTCTC 156
Db 155 TCTGTATCATGCTGATGCTTCTC 177

RESULT 18
ADS18082
ID ADS18082 standard; DNA; 108 BP.

XX AC ADS18082;

XX DT 30-DEC-2004 (first entry)

XX Human/mouse phospholamban transmembrane domain mutant, sense DNA.

XX DE Human; mouse; phospholamban; transmembrane domain; SRL;

XX KW SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;

XX KW sarco(endo)plasmic reticulum calcium ATPase; ss.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Synthetic.

PH Key Location/Qualifiers
FT CDS 19..107
FT /*tag= a
FT /product= "Mutated phospholamban transmembrane domain"

XX US2004203027-A1.
XX 14-OCT-2004.
XX 29-NOV-2003; 2003US-00724532.
XX 02-DEC-2002; 2002US-0430322P.
XX (REED/) REED T D.
XX Reed TD;
XX WPI; 2004-728006/71.

DR P-PSDB; ADS18081.

XX New polypeptide sequence comprising an amino acid substitution, useful as

PT a localisation signal to target therapeutic and experimental compounds or

PT macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic

XX cells.

XX Claim 15; SEQ ID NO 3; 12pp; English.

XX The invention relates to a polypeptide sequence comprising ADS18080 (the

CC transmembrane domain of human/mouse phospholamban) with at least one

CC amino acid substitution at a location selected from L31, N34, F34, L38,

CC L42, V49, or L52. Also included is a nucleic acid encoding the above

CC peptide (appearing as ADS18082-ADS18085). The polypeptide is linked to a

CC compound and/or macromolecule targeted to a sarco(endo)plasmic region of

CC a cell. The polypeptide can be used as a localisation signal to target

CC therapeutic and experimental compounds or macromolecules to the

CC sarco(endo)plasmic reticulum (SR) or eukaryotic cells. The present

CC sequence encodes a mutated transmembrane domain of human/mouse

CC phospholamban which may be used as an SRL (sarco(endo)plasmic

CC localisation signal). The peptide acts as an SRL but is immune to

CC inhibition by sarco(endo)plasmic reticulum calcium ATPase (SERCA).

XX SQ Sequence 108 BP; 21 A; 29 C; 23 G; 35 T; 0 U; 0 Other;

Query Match 28.9%; Score 46; DB 13; Length 108;
Best Local Similarity 65.7%; Pred. No. 0.00034;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 54 TGAATGCCCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 6 TGAGAGAAGCCCTCAGGCCAGGAGAACCTCCAGATGCTTTCATGCTTTTCTGCTGAT 65

Qy 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
Db 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGCTCATGCTCTCT 107

RESULT 19
ADS18083/c
ID ADS18083 standard; DNA; 108 BP.

XX AC ADS18083;

XX DT 30-DEC-2004 (first entry)

XX Human/mouse phospholamban transmembrane domain mutant, antisense DNA.

XX DE Human; mouse; phospholamban; transmembrane domain; SRL;

XX KW SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;

XX KW sarco(endo)plasmic reticulum calcium ATPase; ss.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Synthetic.

PH Key Location/Qualifiers
FT CDS 19..107
FT /*tag= a
FT /product= "Mutated phospholamban transmembrane domain"

XX US2004203027-A1.
XX 14-OCT-2004.
XX 29-NOV-2003; 2003US-00724532.
XX 02-DEC-2002; 2002US-0430322P.
XX (REED/) REED T D.
XX Reed TD;
XX WPI; 2004-728006/71.

XX New polypeptide sequence comprising an amino acid substitution, useful as

PT a localisation signal to target therapeutic and experimental compounds or

PT macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic

PT	cells.
XX	Claim 15; SEQ ID NO 4; 12pp; English.
XX	The invention relates to a polypeptide sequence comprising ADS18080 (the
CC	transmembrane domain of human/mouse phospholamban) with at least one
CC	amino acid substitution at a location selected from I31, N34, F34, I38,
CC	L42, V49, or L52. Also included is a nucleic acid encoding the above
CC	peptide (appearing as ADS18082-ADS18085). The polypeptide is linked to a
CC	compound and/or macromolecule targeted to a sarco(endo)plasmic region of
CC	a cell. The polypeptide can be used as a localisation signal to target
CC	therapeutic and experimental compounds or macromolecules to the
CC	sarco(endo)plasmic reticulum (SR) or eukaryotic cells. A transgene
CC	cassette was constructed for expressing and targeting a peptide to the SR
CC	comprising CaMKII auto inhibitory polypeptide 4 (AIP4), a FLAG epitope
CC	and the SRL of the SR localisation signal of the invention. The present
CC	sequence is the antisense strand for the transgene.
XX	Sequence 108 BP; 35 A; 23 C; 29 G; 21 T; 0 U; 0 Other;
SQ	
Query Match	28.9%; Score 46; DB 13; Length 108;
Best Local Similarity	65.7%; Pred. No. 0.00034;
Matches	67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY	54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db	103 TGAGAGAGGCTCTCAGGCCAGGACCTCCAGAAATGCTTTTGTCTGAT 44
QY	114 CTTATATGCTCTCTGCTCATCTGTATCATCTGATGCTTCT 155
Db	43 TCTCATCTGCTCTGCTCATCTGATTTGCATTATGTCATGCTCTCT 2
RESULT 20	
ADS18085/C	
ID	ADS18085 standard; DNA; 135 BP.
AC	ADS18085;
XX	
DT	30-DEC-2004 (first entry)
XX	
DE	Mouse AIP4-FLAG-SRL transgene antisense DNA.
XX	
KW	FLAG; mouse; phospholamban; transmembrane domain; SRL;
KW	SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;
KW	sarco(endo)plasmic reticulum calcium ATPase; ss; AIP4;
KW	CaMKII auto inhibitory polypeptide 4; transgenic.
XX	
OS	Mus musculus.
OS	Synthetic.
XX	
PN	US2004203027-A1.
XX	
PD	14-OCT-2004.
XX	
XX	29-NOV-2003; 2003US-00724532.
XX	
XX	02-DEC-2002; 2002US-0430322P.
XX	
PA	(REED/) REED T D.
XX	
PI	Reed TD;
XX	
XX	WPI; 2004-728006/71.
XX	
XX	New polypeptide sequence comprising an amino acid substitution, useful as
PT	a localisation signal to target therapeutic and experimental compounds or
PT	macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic
PT	cells.
XX	
XX	Claim 15; SEQ ID NO 6; 12pp; English.
PS	
XX	

CC	The invention relates to a polypeptide sequence comprising ADS18080 (the
CC	transmembrane domain of human/mouse phospholamban) with at least one
CC	amino acid substitution at a location selected from I31, N34, F34, I38,
CC	L42, V49, or L52. Also included is a nucleic acid encoding the above
CC	peptide (appearing as ADS18082-ADS18085). The polypeptide is linked to a
CC	compound and/or macromolecule targeted to a sarco(endo)plasmic region of
CC	a cell. The polypeptide can be used as a localisation signal to target
CC	therapeutic and experimental compounds or macromolecules to the
CC	sarco(endo)plasmic reticulum (SR) or eukaryotic cells. The present
CC	sequence is the antisense strand of a DNA that encodes a mutated
CC	transmembrane domain of human/mouse phospholamban which may be used as an
CC	SRL (sarco(endo)plasmic localisation signal). The peptide acts as an SRL
CC	but is immune to inhibition by sarco(endo)plasmic reticulum calcium
CC	ATPase (SERCA).
XX	Sequence 135 BP; 38 A; 34 C; 32 G; 31 T; 0 U; 0 Other;
SQ	
Query Match	28.9%; Score 46; DB 13; Length 135;
Best Local Similarity	65.7%; Pred. No. 0.00036;
Matches	67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY	54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCAT 113
Db	118 TGAGAGAGGCTCTCAGGCCAGGACCTCCAGAAATGCTTTTGTCTGAT 59
QY	114 CTTAATATGCTCTTCTGCTGATCTGTATCATCTGATGCTTCT 155
Db	58 TCTCATCTGCTCTCTGCTGATTTGCATTATGTCATGCTGATGCTCT 17
RESULT 21	
ADS18084	
ID	ADS18084 standard; DNA; 135 BP.
XX	
AC	ADS18084;
XX	
DT	30-DEC-2004 (first entry)
XX	
DE	Mouse AIP4-FLAG-SRL transgene sense DNA.
XX	
KW	FLAG; mouse; phospholamban; transmembrane domain; SRL;
KW	SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;
KW	sarco(endo)plasmic reticulum calcium ATPase; ss; AIP4;
KW	CaMKII auto inhibitory polypeptide 4; transgenic.
XX	
OS	Mus musculus.
OS	Synthetic.
XX	
PN	US2004203027-A1.
XX	
PD	14-OCT-2004.
XX	
XX	29-NOV-2003; 2003US-00724532.
XX	
XX	02-DEC-2002; 2002US-0430322P.
XX	
PA	(REED/) REED T D.
XX	
PI	Reed TD;
XX	
XX	WPI; 2004-728006/71.
XX	
XX	New polypeptide sequence comprising an amino acid substitution, useful as
PT	a localisation signal to target therapeutic and experimental compounds or
PT	macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic
PT	cells.
XX	
XX	Claim 15; SEQ ID NO 5; 12pp; English.
PS	
XX	

Db	1215	ATCACAGGAATTCACCACTTTATCAGCTTCAAGAGCATTTTATCAGCAGCATCCA	1274
Qy	94	TTTATCAATTCGTCTCATCTTAATATGCTCTTGTGATCTGT	138
Db	1275	TGTTTAACTTTTGTCTTTTCAATTAAGTGAAACATATGAACCTGT	1319
RESULT 25			
ABL34196/c	ABL34196 standard; DNA; 37973 BP.		
XX	AC	ABL34196;	
XX	AC		
DT	26-MAR-2002	(first entry)	
XX	Human	immune system associated gene SEQ ID NO: 2169.	
DE	Human	immune system disease; cytosine methylation; antiasthmatic;	
XX	Human	immune system disease; cytosine methylation; antiasthmatic;	
KW	antiasthmatic; anti-HIV; anticonvulsant; ophthalmological;		
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;		
KW	antiasthmatic; antiarthritic; antidiabetic; antipsoriatic;		
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;		
XX	ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200200928-A2.		
XX	03-JAN-2002.		
XX	02-JUL-2001; 2001WO-EP007537.		
XX	30-JUN-2000; 2000DE-01032529.		
XX	01-SEP-2000; 2000DE-01043826.		
XX	(EPIG-) EPIGENOMICS AG.		
PA	Olek A, Piepenbrock C, Berlin K;		
XX	WPI; 2002-130909/17.		
XX	Nucleic acid comprising fragment of chemically modified gene, useful for		
PT	diagnosis and treatment of diseases associated with abnormal cytosine		
PT	methylation.		
XX	Claim 1; SEQ ID NO 2169; 32pp + Sequence Listing; German.		
XX	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention		
XX	Sequence 37973 BP; 10166 A; 620 C; 8741 G; 18446 T; 0 U; 0 Other;		
SQ	Query Match	21.0%; Score 33.4; DB 6; Length 37973;	
	Best Local Similarity	62.7%; Pred. No. 15;	
	Matches	52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;	
Qy	72	ACGTCAAAGCTACAGAACTATTATTCATTTCTGCTCATCTTAATATGCTCTTGTCT	131
Db	12130	ACTTCACATTATAAAATATATTATCTATAATTTCTTTCTTAATATCTTTCTCT	12071
Qy	132	GATCTGTATCATCGTGTGCTTC	154
Db	12070	AATTTTAAACAAAATAATAC	12048

CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 170279 BP; 51527 A; 31503 C; 31927 G; 54249 T; 0 U; 1073 Other;

Query Match 20.5%; Score 32.6; DB 13; Length 170279;
Best Local Similarity 51.7%; Pred. No. 41;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 15 ATACCTCACTCGCTCAGCTATAGAGAGCCCTCAACCAATTGAATGCTTCAACAGCAGC 74
Db 142522 AAAGCTCACCATTCTTTGTTATGATATAGCTCAGTTCTTGCATGACTTAACCTGATCACA 142463

QY 75 TCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATATGCTCTTGTGTGAT 134
Db 142462 GAATAAGCTGCAGTATATATGCAACACTTAATTTGTTTCATGCTGTTCCACTGCCCT 142403

QY 135 CTGTATCATCGTGATGCTTCTCT 157
Db 142402 TTATTTCTTATTGTTTGACCTCT 142380

RESULT 28
AAQ64111/C
ID AAQ64111 standard; DNA; 3713 BP.
XX
AC AAQ64111;
XX
DT 02-FEB-1995 (first entry)
XX
DE cryET4 gene.
XX
KW cryET4; cryET5; Lepidoptera; lepidopteran insect; insecticidal; toxin;
KW insecticidal crystal protein; ICP; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 99..3602
FT /*tag= a
FT /note= "claim 2"
XX
PN US5322687-A.
XX
XX 21-JUN-1994.
XX
XX 29-JUL-1993; 93US-00100709.
XX
XX 29-JUL-1993; 93US-00100709.
XX
XX (ECOG-) ECOGEN INC.
XX
XX Tan Y, Jany CS, Donovan WP, Gonzalez JM;
XX
XX WPI; 1994-199503/24.
XX P-PSDB; AAR54073.
XX
XX Isolated cryET4 gene and Bacillus thuringiensis cultures transformed with
XX this gene - used in compsns. against lepidopteran insects.
XX
XX

PS Claim 2; Col 15-24; 51pp; English.
XX
CC B. thuringiensis strain EG5847 exhibits insecticidal activity against
CC lepidopteran insects. Two novel toxin genes from B. thuringiensis EG5847
CC designated cryET4 and cryET5 produce insecticidal proteins with activity
CC against a broad spectrum of lepidopteran insects. The gene sequences are
CC given in AAQ64111-12
XX
SQ Sequence 3713 BP; 1253 A; 609 C; 802 G; 1049 T; 0 U; 0 Other;

Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 17;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCATCTTAATATGCTCTTGTGCTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTGATTAATTTCTCCCTAATCTTCTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
Db 381 CTTTGTCTTACTGTGTTCTTCTAT 357

RESULT 29
AAT95050/C
ID AAT95050 standard; DNA; 3713 BP.
XX
AC AAT95050;
XX
DT 17-FEB-1998 (first entry)
XX
DE DNA encoding Bacillus thuringiensis crystal toxin cryET4.
XX
KW EG7279; crystal toxin; cryET4; lepidopteran pest; Heliothis virescens;
KW Helicoverpa zea; Lymantria dispar; Ostrinia nubilalis;
KW Pseudoplusia includens; Plutella xylostella; Spodoptera exigua;
KW Spodoptera frugiperda; Trichoplusia ni; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 99..3602
FT /*tag= a
FT /product= "CryET4"
XX
PN US5679343-A.
XX
XX 21-OCT-1997.
XX
XX 07-JUN-1995; 95US-00474038.
XX
XX 29-JUL-1993; 93US-00100709.
XX 30-DEC-1993; 93US-00176865.
XX
XX (MONS) MONSANTO CO.
XX
XX Jany CS, Gonzalez JM, Donovan WP, Tan Y;
XX
XX WPI; 1997-525682/48.
XX P-PSDB; AAW35250.
XX
XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
XX control Lepidopteran pests.
XX
XX Example 2; Col 15-24; 50pp; English.
XX
XX The present sequence encodes the Bacillus thuringiensis EG7279 crystal
XX toxin cryET4, which, optionally in association with B. thuringiensis
XX EG7279, can be used against lepidopteran pests. cryET4 is especially
XX useful for controlling Heliothis virescens, Helicoverpa zea, Lymantria
XX dispar, Ostrinia nubilalis, Pseudoplusia includens, Plutella xylostella,
XX Spodoptera exigua, Spodoptera frugiperda and Trichoplusia ni
XX

SQ Sequence 3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;
 Query Match 20.3%; Score 32.2; DB 2; Length 3713;
 Best Local Similarity 61.2%; Pred. No. 17;
 Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 73 CGTCAAAAGCTACAGAAATCATTTATTCATTTCTGTCTCATCTTAATATGTCCTCTGCG 132
 Db 441 CTTTAAATGCTTCAGCGTATATTGATAATTTCTCCCTAATCCCTTAATTCAGTGATTG 382
 QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
 Db 381 CTTTGTCTTACTGTGTGCTTCTAT 357
 RESULT 30
 AAT68435/C
 ID AAT68435 standard; DNA; 3713 BP.
 XX AC AAT68435;
 XX DT 25-MAR-2003 (revised)
 DT 07-JUL-1997 (first entry)
 XX DE CryET4 gene.
 KW CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal protein;
 KW ICP; toxin; CryI protein; lepidopteran insect; insecticide; ds.
 XX OS Bacillus thuringiensis.
 FH Key Location/Qualifiers
 FT CDS 99..3602
 FT /*tag= a
 FT /product= "cryET4"
 XX US5616319-A.
 PD 01-APR-1997.
 PF 30-DEC-1993; 93US-00176865.
 PR 29-JUL-1993; 93US-00100709.
 PA (MONS) MONSANTO CO.
 FI Gonzalez JM, Donovan WP, Tan Y, Jany CS;
 FI WPI; 1997-212077/19.
 DR P-PSDB; AAW17700.
 XX
 FT Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful
 FT for control of lepidopteran pests.
 XX
 PS Example 3; Col 15-24; 50pp; English.
 XX
 CC This sequence represents the cryET4 gene of Bacillus thuringiensis (B.t.)
 CC isolate BG5847. B.t. produces inclusions during sporulation which include
 CC insecticidal crystal proteins (ICP). ICP toxins are active in insects
 CC only after ingestion. Once ingested, the toxic components disrupt the
 CC midgut cells, resulting in cessation of feeding, and eventually death.
 CC The CryI proteins produced by B.t. are active against lepidopteran
 CC insects. The protein encoded by this sequence, and the CryET5 protein
 CC (see AAW17699) belong to the CryI family of ICPs. This sequence can be
 CC used to transform bacteria, which are useful as insecticides against a
 CC wide range of lepidopteran pests, and can be applied to crops, soil and
 CC seeds. The encoded protein, or especially its toxic N terminal region,
 CC can be expressed in plants, to provide protection against lepidopteran
 CC pests. This sequence, or its fragments, can also be used to isolate other
 CC similar genes. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;

Db 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATCTTCTTAATTCAGTGATTG 382

Qy 133 ATCTGTATCATCGTGCATGCTTCTCT 157

Db 381 CTTTGTCTTACTGTGCTTCTAT 357

RESULT 32

AAZ09159/c

ID AAZ09159 standard; DNA; 3713 BP.

XX

AC AAZ09159;

XX

DT 18-OCT-1999 (first entry)

XX

DE B. thuringiensis cryET4 toxin DNA.

XX

KW Toxin; cryET4; cryET5; insecticidal; Lepidoptera; transformed plant;

KW crystal protein; insect; ds.

XX

OS Bacillus thuringiensis.

XX

XX Key Location/Qualifiers

FT CDS 99..3602

FT /*tag= a

FT /product= "cryET4"

XX

XX US5942658-A.

XX

XX 24-AUG-1999.

XX

XX 24-JUN-1997; 97US-00881340.

XX

XX 29-JUL-1993; 93US-00100709.

PR 30-DEC-1993; 93US-00176865.

PR 07-JUN-1995; 95US-00474038.

XX

PA (MONS) MONSANTO CO.

XX

XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;

XX

XX WPI; 1999-493544/41.

DR P-PSDB; AAY30922.

XX

PT Transformed plant comprising insecticidal crystal proteins.

XX

PS Claim 2; Fig 1A-J; 50pp; English.

XX

CC This invention describes novel transformed plants containing Bacillus

CC thuringiensis strain BG5847 insecticidal crystal protein genes cryET4 or

CC cryET5. cryET4 and cryET5 are novel toxin genes which produce

CC insecticidal proteins with activity against a broad spectrum of insects

CC of the order Lepidoptera. This sequence encodes the cryET4 protein

CC described in the method of the invention

XX

XX Sequence 3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;

SQ

Query Match 20.3%; Score 32.2; DB 2; Length 3713;

Best Local Similarity 61.2%; Pred. No. 17;

Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 73 CGTCAAAAGCTACAGATCTATTTATCAATTTCTGCTCATCTTAATATGCTCTTCTG 132

Db 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATCTTCTTAATTCAGTGATTG 382

Qy 133 ATCTGTATCATCGTGCATGCTTCTCT 157

Db 381 CTTTGTCTTACTGTGCTTCTAT 357

RESULT 33

ADO43653/c

ID ADO43653 standard; DNA; 127432 BP.

XX

AC ADO43653;

XX

DT 29-JUL-2004 (first entry)

XX

DE Nucleotide sequence of BAC-64.

XX

KW pentatricopeptide sequence; PPR sequence; ppr-A; ppr-B; ppr-C;

KW male fertility; plant; Rfo locus; radish; Brassica; cytoplasmic inducer;

KW BAC; primer; ss.

XX

OS Synthetic.

XX

PN WO2004039988-A1.

XX

PD 13-MAY-2004.

XX

PF 29-OCT-2003; 2003WO-FR003224.

XX

PR 29-OCT-2002; 2002FR-00013512.

XX

XX (GENO-) GENOPLANTE-VALOR.

PA

XX Budar F, Giancola S, Bendahmane A, Desloire S, Delourme R;

PI Marhadour S, Falentin-Guyomarc'h H, Falentin C, Renard M, Gherbi H;

PI Laloui W, Bonden S, Wilmer J, Clouet V;

XX

DR WPI; 2004-376197/35.

XX

XX New pentatricopeptides from plants, useful for restoration of male

PT fertility in Brassica containing cytoplasmic inducer of male sterility,

PT especially for production of colza hybrids, also related nucleic acids.

XX

XX Example 1; Page 67-102; 106pp; French.

XX

XX The present sequence represents bacterial artificial chromosome (BAC)-64.

CC This BAC contains the Rfo locus, which contains pentatricopeptide (PPR)

CC sequences. The specification describes PPR sequences, designated ppr-A,

CC ppr-B and ppr-C. These PPR sequences are able to restore male fertility

CC in plant. PPR sequences, used singly or in combination, are used to

CC restore male fertility in Brassica, specifically B. napus, that contain a

CC cytoplasmic inducer of male sterility. The plants with restored fertility

CC are used for production of hybrids.

XX

SQ Sequence 127432 BP; 42300 A; 21940 C; 21537 G; 40004 T; 0 U; 1651 Other;

Query Match 20.3%; Score 32.2; DB 12; Length 127432;

Best Local Similarity 50.3%; Pred. No. 50;

Matches 76; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 7 AAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCGCTCAACCATTTGAATGCCCTCAA 66

Db 13865 AAAGTCNAGAAGCATATCTCCGTTTCMAAATCCAGCTTCAATAATACATCTGAGA 13806

Qy 67 CAAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGCTCATCTTAATATGCTC 126

Db 13805 AAAGTACCTCCACTTTTCTTAGCTTACATTTCTTCTTCTTCTTCTTCTTCTTCT 13746

Qy 127 TTGCTGATCTGATCATCGTGATGCTTCTCT 157

Db 13745 CATAGANGCAGTGTCTGCAAACTTCTTCTTCT 13715

RESULT 34

ADN73394/c

ID ADN73394 standard; cDNA; 1590 BP.

XX

AC ADN73394;

XX

DT 15-JUL-2004 (first entry)

XX

DE Thale cress cDNA upregulated in E2Pa/Dpa expressing plants SeqID 1289.

XX KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
XX KW growth regulator; animal feed product; thale cress;
XX KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
XX OS Arabidopsis thaliana.
XX FN WO2004035798-A2.
XX PD 29-APR-2004.
XX XX 20-OCT-2003; 2003WO-EP011658.
XX PF 18-OCT-2002; 2002EP-00079408.
XX XX (CROP-) CROPDISEIGN NV.
XX PA Inze D, De Veylder L, Vlieghe K;
XX PI WPI; 2004-348466/32.
XX DR P-PSDB; ADN73395.
XX XX Altering plant characteristics, useful for producing plants for enzyme or
XX PT pharmaceutical production comprises modifying in a plant, expression of
XX PT one or more nucleic acids and/or modifying level or activity of one or
XX PT more proteins.
XX PS Claim 1; SEQ ID NO 1289; 134pp; English.
XX XX This invention relates to a novel method for altering one or more plant
XX CC characteristics. Specifically, it refers to identifying genes that are up
XX CC - or down-regulated in transgenic plants overexpressing the heterodimeric
XX CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
XX CC alter plant characteristics accordingly. The present invention describes
XX CC generating transgenic plants for the production of growth regulators,
XX CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
XX CC the altered plant characteristics are selected from increased yield or
XX CC biomass, enhanced survival capacity, stress tolerance, plant architecture
XX CC or physiology, altered endoreplication, biochemistry, signal
XX CC transduction, storage lipid mobilisation and/or altered photosynthesis,
XX CC each relative to the corresponding wild type plants. Accordingly, these
XX CC sequences can also be useful as positive or negative selectable markers
XX CC during transformation of cells or tissues. The identified genes play a
XX CC role in a variety of biological processes such as DNA replication, cell
XX CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
XX CC transcription factors. This polynucleotide sequence is thale cress cDNA
XX CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
XX CC transcription factor, given in an exemplification of the invention.
XX SQ Sequence 1590 BP; 440 A; 289 C; 442 G; 419 T; 0 U; 0 Other;
Query Match 20.1%; Score 32; DB 12; Length 1590;
Best Local Similarity 51.4%; Pred. No. 15;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 13 CAATACCTCACTCGCTCAGCTATAAGAGAGCGCTCAACCATTCGATCAACAGCA 72
Db 1449 CAGCTCCACCGCGCTCTATTCAGATGCTCAGAACCAATATGCCAGGATAAC 1390
QY 73 CGTCAAAAGCTACAGAACTATTATTAATTTCTGCTCATCTTAATATGCTCTCTGCTG 132
Db 1389 AGCAACAAGCTGAAGACTGTAGAGACCTGATTCAGCTTCGAGATTATTTCTCATCTTC 1330
QY 133 ATCTGTATCATCGTGTGCTTCTC 156
Db 1329 ATCCAACCTCAAGGTCAATCAAGCTC 1306
RESULT 35
ID AAV74594
XX AAV74594 standard; DNA; 1421 BP.
AC AAV74594;

XX 16-MAR-1999 (first entry)
XX Staphylococcus aureus contig SEQ ID #283.
DE Computer readable medium; vaccine; S.aureus infection; immunodetection;
XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX KW skin infection; surgical wound infection; scalded skin syndrome;
XX KW toxic shock syndrome; ds.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
XX FT misc_feature 481..540
XX FT /*tag= a
XX FT the sequence listing in the specification. They are
XX FT included to maintain the nucleotide numbering given in
XX FT the specification for this DNA sequence"
XX PN EP786519-A2.
XX XX 30-JUL-1997.
XX PD 07-JAN-1997; 97EP-00100117.
XX PF 05-JAN-1996; 96US-0009861P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX PI WPI; 1997-374922/35.
XX DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX XX stored on computer readable medium and used in the production of anti-
XX PT S.aureus vaccines.
XX PS Claim 1; Page 1107-1108; 3271pp; English.
XX XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
XX CC of the invention. The DNA sequences are recorded on a computer readable
XX CC medium, preferably selected from a floppy or hard disk, random access
XX CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
XX CC the S.aureus DNA sequences allows putative functions to be assigned so
XX CC that protein-encoding or regulatory regions of commercial, therapeutic or
XX CC industrial importance can be obtained. Specifically, sequences which are
XX CC likely to encode antigens have been identified and these polypeptides can
XX CC be used in a vaccine composition against S.aureus infection. The
XX CC polypeptides can also be used in a kit for the immunodetection of
XX CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
XX CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
XX CC skin and surgical wound infections, scalded skin syndrome, toxic shock
XX CC syndrome, etc. Organisms transformed with the DNA sequences can be used
XX CC for recombinant production of the polypeptides. The new DNA sequences
XX CC (and their fragments) are useful as primers or probes for isolating
XX CC homologues of any of the S.aureus DNA sequences contained on the computer
XX CC readable medium
XX SQ Sequence 1421 BP; 506 A; 174 C; 258 G; 422 T; 0 U; 61 Other;
Query Match 20.0%; Score 31.8; DB 2; Length 1421;
Best Local Similarity 61.4%; Pred. No. 17;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 36 AAGAAGCGCTCAACCATTCGAATGCTTCAACAGCAGCTCAACAGCTACAGATCTATT 95
Db 317 ACGAAGAAGCTCAACCATTCGAATGCTTCAACAGCAGCTCAACAGCTACAGATCTATT 376
QY 96 TATCAATTTCTCTCTCATCTTAA 118
Db 377 CTTCAATTACTCTTATAAATAAA 399

XX AAS69551;
AC
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #5355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX PD
XX 30-MAR-2001; 2001WO-US008631.
XX PF
XX 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX XX (HYSE-) HYSEQ INC.
XX PA Drmanac RT, Liu C, Tang YT;
XX PI P-PSDB; ABG05364.
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG05364.
XX XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 5355; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful for treating disorders
CC of sites expressing (II). (I) and (II) are useful for biological actions. The
CC involving aberrant protein expression or biological actions in
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 873 BP; 235 A; 191 C; 229 G; 218 T; 0 U; 0 Other;
SQ
Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 37 AGAAGAGCCCTCAACCATTTGAAATGCCCTCAACAGACGCTCAAAAGCTACAGAAATCTATT 96
DB 207 AAAGAAACATATACCATTAATAAATTCATATAGGTATTAATATCTTCCCAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTTAATATGCTCTTGTGTGATCTGTATCATCGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 88
QY 157 T 157

XX
AC
DT ADW94142 standard; DNA; 6025 BP.
XX
AC ADW94142;
XX
DT 21-APR-2005 (first entry)
XX
DE Staphylococcus aureus proliferation-required operon, SEQ ID 76.
XX
KW Operon; cell proliferation; microorganism; ds.
XX
OS Staphylococcus aureus.
XX
XX US2005026189-A1.
XX PN
XX 03-FEB-2005.
XX PD
XX 28-MAY-2004; 2004US-00857625.
XX PF
XX 29-MAY-2003; 2003US-0474768P.
XX PR
XX (WANG/) WANG L.
XX PA (ZAMU/) ZAMUDIO C.
XX PI Wang L, Zamudio C;
XX XX
XX WPI; 2005-151156/16.
XX DR
XX Predicting operons of prokaryotes, by segregating consecutive genes of
XX organism, into bins based on their orientation, performing composite
XX operon prediction analysis, associating genes between operon boundaries
XX as putative operons.
XX
XX Example 7; SEQ ID NO 76; 116pp; English.
XX
XX The present invention relates to a method (M1) for predicting operons of
CC target prokaryotes. The method comprises identifying consecutive genes of
CC an organism's genome, determining the orientation of a gene in the genome
CC relative to its flanking genes, segregating the genes into bins based on
CC their orientation, performing composite operon prediction analysis,
CC determining operon boundaries by identifying gene pairs with confidence
CC scores below specific threshold and associating genes between boundaries
CC as putative operons. Also claimed is a computer-based system (I) for
CC carrying out (M1). (M1) is useful for identifying a gene that is required
CC for proliferation of a microorganism and in cell-based assays. ADW94067-
CC ADW94260 are proliferation-required operons from Staphylococcus aureus,
CC predicted using the method of the invention. ADW94261-ADW94610 are
CC proliferation-required genes, and ADW94611-ADW94884 are the encoded
CC proteins, from the predicted operons of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20050026189.
XX
XX Sequence 6025 BP; 2262 A; 783 C; 1086 G; 1894 T; 0 U; 0 Other;
SQ
Query Match 20.0%; Score 31.8; DB 14; Length 6025;
Best Local Similarity 61.4%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 36 AAGAAGAGCCCTCAACCATTTGAAATGCCCTCAACAGACGCTCAAAAGCTACAGATCTATT 95
DB 2301 ACGAAGAAACTGAAATTTTGAATTTGGGTGGATATCATGTCAAATATATGTCAGATGTA 2360
QY 96 TATCAATTTCTGTCTCATCTTAA 118
DB 2361 CTTCAATTAATCTATAAAATAA 2383
RESULT 37
AAS69551/C
ID AAS69551 standard; cDNA; 873 BP.

Db 87 T 87

RESULT 38
AAS69244/c
ID AAS69244 standard; cDNA; 873 BP.
XX
XX AAS69244;
AC
XX
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #5048.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG05057.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 5048; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 37 AGAAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAACAGCTCAAGATCTATT 96
DB 207 AAAGAAACATACCACTTAAATAAATTCATATAGGTATTAAATCTTCCCAATCATC 148

QY 97 ATCAATTCTGCTCATCTTAATATGCTCTTCTGATCTGATCATCATGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88

QY 157 T 157
DB 87 T 87

RESULT 39
AAS75469/c
ID AAS75469 standard; cDNA; 873 BP.
XX
XX AAS75469;
AC
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #11273.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG11282.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 11273; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 37 AGAAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAACAGCTCAAGATCTATT 96
DB 207 AAAGAAACATACCACTTAAATAAATTCATATAGGTATTAAATCTTCCCAATCATC 148

Db 2510 TTGAGTTATATTAAGAATTTCTTTAAATATATATTTAAGATATCTTTCTGTCAGAGTA 2569
142 A 142
2570 A 2570

RESULT 42
ABL32288/c
ID ABL32288 standard; DNA; 5875 BP.
XX AC ABL32288;
XX DT 26-MAR-2002 (first entry)
XX DE Human immune system associated gene SEQ ID NO: 261.
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianemic; cytotatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX OS Homo sapiens.
XX PN WO200200928-A2.
XX PD 03-JAN-2002.
XX PF 02-JUL-2001; 2001WO-EP007537.
XX PR 30-JUN-2000; 2000DE-01032529.
XX PX 01-SEP-2000; 2000DE-01043826.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX DR Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX PS Claim 1; SEQ ID NO 261; 32pp + Sequence Listing; German.
XX CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX SQ Sequence 5875 BP; 1930 A; 27 C; 1031 G; 2887 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 6; Length 5875;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 21 CACTCGCTCAGCTATAGAAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAA 80
421 CATACTTTCTCTTTAAATAAATACTAAATTAATTTCACTTCAACACCACTTCAAAA 362

QY 81 GCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCT 125
361 ACTACTCACTATTTTCTAAATTAATTTCCCCCATAAATTTCT 317

Db

RESULT 43
ACN44322/c
ID ACN44322 standard; DNA; 84073 BP.
XX AC ACN44322;
XX DT 18-NOV-2004 (first entry)
XX DE Human genomic sequence HCG28354.
XX KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX OS Homo sapiens.
XX PN WO2003073826-A2.
XX PD 12-SEP-2003.
XX PF 28-FEB-2003; 2003WO-US006235.
XX PX 01-MAR-2002; 2002US-00087192.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW;
XX WPI; 2003-328604/31.
XX DR Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX PS Claim 1; SEQ ID NO 712; Opp; English.
XX CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX SQ Sequence 84073 BP; 25133 A; 15743 C; 16036 G; 27161 T; 0 U; 0 Other;
Query Match 19.6%; Score 31.2; DB 11; Length 84073;
Best Local Similarity 58.7%; Pred. No. 89;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 37 AGAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAAGCTCAGAGATCTATTT 96
28668 AGTAGAGATACAGCCACACAAAGAATCCAGGCTCACATAAAACCAACAGAGATTATCT 28609

Db

QY 97 ATCAATTTCTGCTCATCTTAATATGCTCTT 128
28608 AACAACTTTGAATCTTGTATCTGAGTCTT 28577

Db

RESULT 44
ADR60594/c
ID ADR60594 standard; cDNA; 1269 BP.
XX AC ADR60594;
XX DT 02-DEC-2004 (first entry)
XX DE Cotton cDNA sequence, SEQ ID 1475.

XX KW nuclear fertility; plant; male-fertility; male-fertility restorer;
KW marker; transformation; radish; Rfo; petunia; Rf; Brassica napus; ds;
XX gene.
XX OS Raphanus sativum.
XX PN WO2004006655-A2.
XX XX
XX PD 22-JAN-2004.
XX XX
XX PF 16-JAN-2003; 2003WO-US001343.
XX PR 12-JUL-2002; 2002US-00195144.
XX PR 15-JAN-2003; 2003US-00345072.
XX XX
XX PA (UYMC-) UNIV MCGILL.
XX PA (DNAL-) DNA LANDMARKS INC.
XX PA (BADI) BASF PLANT SCI GMBH.
XX XX
XX PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;
XX PI Lai FW, Leforest M;
XX XX
XX DR WPI; 2004-122713/12.
XX XX
XX PT Using a plant male-fertility restorer as a marker for transformation by
XX PT providing an expression cassette encoding a plant male fertility restorer
XX PT and transforming cytoplasmic male sterile plant cells with the expression
XX PT cassette.
XX XX
XX PS Claim 15; SEQ ID NO 87; 309pp; English.
XX XX
XX CC The invention relates to a novel method for using a plant male-fertility
XX CC restorer as a marker for transformation. Using a plant male-fertility
XX CC restorer as a marker for transformation comprises: providing an
XX CC expression cassette for a male fertility restorer; transforming an
XX CC cytoplasmic male sterile plants with the expression cassette; and
XX CC identifying plants from step (2) that form seeds when self-pollinated.
XX CC The male fertility restorer is a radish Rfo or a petunia Rf. The plant is
XX CC Brassica napus. The expression cassette is covalently linked to a
XX CC sequence of interest. The expression cassette is co-transformed into the
XX CC plant cells with a nucleotide sequence of interest. The method is useful
XX CC for using a plant male-fertility restorer as a marker for transformation.
XX CC The present sequence is used in the exemplification of the invention.
XX XX
XX SQ Sequence 271990 BP; 89601 A; 47321 C; 46931 G; 88077 T; 0 U; 60 Other;
XX XX
XX Query Match 19.5%; Score 31; DB 12; Length 271990;
XX Best Local Similarity 53.8%; Pred. No. 1.5e+02;
XX Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
XX QY 7 AAAGTCCAAATACCTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTCGCTCAA 66
XX Db 94279 AAAGTCAAGAAGCAATATCTCGTTTCAAAATCCAGCTTCAATATCAATCCTGAGA 94220
XX QY 67 CAAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCT 125
XX Db 94219 AAAGTACCTCCACTTTTCTAGCTTACATTCGCTCAATTTCTTCTTCTTAATCAGTTT 94161
XX XX
XX RESULT 48
XX ADN61228/c
XX ID ADN61228 standard; cDNA; 437 BP.
XX XX
XX AC ADN61228;
XX XX
XX XX 02-DEC-2004 (first entry)
XX XX
XX DE Cotton cDNA sequence, SEQ ID 1993.
XX XX
XX KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
XX KW drought tolerance; plant disease resistance; galactomannan; lignin;
XX KW plant growth regulator; heat tolerance; herbicide tolerance;
XX XX

XX KW nuclear fertility; plant; male-fertility; male-fertility restorer;
KW marker; transformation; radish; Rfo; petunia; Rf; Brassica napus; ds;
XX gene.
XX OS Raphanus sativum.
XX PN WO2004006655-A2.
XX XX
XX PD 22-JAN-2004.
XX XX
XX PF 16-JAN-2003; 2003WO-US001343.
XX PR 12-JUL-2002; 2002US-00195144.
XX PR 15-JAN-2003; 2003US-00345072.
XX XX
XX PA (UYMC-) UNIV MCGILL.
XX PA (DNAL-) DNA LANDMARKS INC.
XX PA (BADI) BASF PLANT SCI GMBH.
XX XX
XX PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;
XX PI Lai FW, Leforest M;
XX XX
XX DR WPI; 2004-122713/12.
XX XX
XX PT Using a plant male-fertility restorer as a marker for transformation by
XX PT providing an expression cassette encoding a plant male fertility restorer
XX PT and transforming cytoplasmic male sterile plant cells with the expression
XX PT cassette.
XX XX
XX PS Claim 15; SEQ ID NO 87; 309pp; English.
XX XX
XX CC The invention relates to a novel method for using a plant male-fertility
XX CC restorer as a marker for transformation. Using a plant male-fertility
XX CC restorer as a marker for transformation comprises: providing an
XX CC expression cassette for a male fertility restorer; transforming an
XX CC cytoplasmic male sterile plants with the expression cassette; and
XX CC identifying plants from step (2) that form seeds when self-pollinated.
XX CC The male fertility restorer is a radish Rfo or a petunia Rf. The plant is
XX CC Brassica napus. The expression cassette is covalently linked to a
XX CC sequence of interest. The expression cassette is co-transformed into the
XX CC plant cells with a nucleotide sequence of interest. The method is useful
XX CC for using a plant male-fertility restorer as a marker for transformation.
XX CC The present sequence is used in the exemplification of the invention.
XX XX
XX SQ Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;
XX XX
XX Query Match 19.5%; Score 31; DB 10; Length 271990;
XX Best Local Similarity 53.8%; Pred. No. 1.5e+02;
XX Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
XX QY 7 AAAGTCCAAATACCTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTCGCTCAA 66
XX Db 94279 AAAGTCAAGAAGCAATATCTCGTTTCAAAATCCAGCTTCAATATCAATCCTGAGA 94220
XX QY 67 CAAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCT 125
XX Db 94219 AAAGTACCTCCACTTTTCTAGCTTACATTCGCTCAATTTCTTCTTCTTAATCAGTTT 94161
XX XX
XX RESULT 47
XX ADN61228/c
XX ID ADN61228 standard; cDNA; 271990 BP.
XX XX
XX AC ADN61228;
XX XX
XX XX 01-JUL-2004 (first entry)
XX XX
XX DE Radish nuclear fertility restorer Rfo locus SEQ ID NO:87.
XX XX

KW	homologous recombination; extreme osmotic condition tolerance;	
KW	pathogen resistance; pest resistance; yield; photosynthesis; seed oil;	
KW	stress resistance.	
XX		
OS	Gossypium hirsutum.	
XX		
PN	US2004181830-A1.	
XX		
PD	16-SEP-2004.	
XX		
XX	29-JAN-2004; 2004US-00767795.	
PF		
XX	07-MAY-2001; 2001US-00849529.	
PR		
PR	12-DEC-2001; 2001US-00021323.	
XX		
XX	(KOVA/) KOVALIC D K.	
PA	(ZHOU/) ZHOU Y.	
PA	(CAO/) CAO Y.	
XX		
PI	Kovalic DK, Zhou Y, Cao Y;	
XX		
DR	WPI; 2004-667718/65.	
XX		
XX	New recombinant nucleic acid molecules and polypeptides from Gossypium	
PT	hirsutum, useful for producing plants with improved biological	
PT	characteristics (e.g. improved plant cold or drought tolerance).	
PT		
XX		
XX	Claim 1; SEQ ID NO 1993; 14pp; English.	
PS		
CC	The invention relates to a recombinant polynucleotide comprising any of	
CC	the 58798 Cotton plant cDNA sequences mentioned in the specification.	
CC	Also a recombinant polypeptide comprising any of the 58798 amino acid	
CC	sequences mentioned in the specification and producing a plant having an	
CC	improved property. Producing a plant having an improved property	
CC	comprises transforming a plant with a recombinant construct comprising a	
CC	promoter region functional in a plant cell operably joined to a	
CC	polynucleotide comprising a coding sequence for a polypeptide associated	
CC	with the property, and growing the transformed plant. The polypeptide is	
CC	useful for improving plant cold tolerance, manipulating growth rate in	
CC	plant cells by modification of the cell cycle pathway, improving plant	
CC	drought tolerance, providing increased resistance to plant disease,	
CC	producing galactanmanan (or lignin or plant growth regulators), improving	
CC	plant heat tolerance, improving plant tolerance to herbicides, increasing	
CC	the rate of homologous recombination in plants, improving plant tolerance	
CC	to extreme osmotic conditions or to pathogens or pests, improving yield	
CC	by modification of photosynthesis, modifying seed oil or protein yield	
CC	and/or content, improving yield by modification of carbohydrate, nitrogen	
CC	or phosphorus use and/or uptake, or improving yield by providing improved	
CC	plant growth and development under at least one stress condition. The	
CC	polynucleotide and polypeptide may also be used in recombinant DNA	
CC	constructs, in physical arrays of molecules, as plant breeding markers,	
CC	or in computer-based storage and analysis systems. The present sequence	
CC	is a Cotton plant cDNA of the invention. NOTE: The sequence data for this	
CC	patent did not form part of the printed specification, but was obtained	
CC	in electronic format directly from USPTO at	
CC	seqdata.uspto.gov/sequences.html?DocID=20040181830. However only 6585	
CC	polynucleotide sequences were available, the remaining 52213	
CC	polynucleotides and all 58798 protein sequences were not present.	
XX		
SQ	Sequence 437 BP; 150 A; 58 C; 119 G; 110 T; 0 U; 0 Other;	
	Query Match 19.4%; Score 30.8; DB 13; Length 437;	
	Best Local Similarity 54.4%; Pred. No. 24;	
	Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	
QY	28 TCAGCTATAGAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAG 87	
DB	311 TGATCTAAATTTGAATCAGGATCAATTCAGAGGAATCAACAATTTCTTCGAAATACAC 252	
QY	88 AATCTATTTATCAATTTTGTCTCATCTTAATATGTTCTTTGCTGATCTGTATC 141	
DB	251 CAATATATTGGACATCCATCCATTTTCTTGTCTTCTTGTCTTCCCAATACC 198	

RESULT 49	
AAQ62612	
ID	AAQ62612 standard; DNA; 2090 BP.
XX	
AC	AAQ62612;
XX	
XX	25-MAR-2003 (revised)
DT	17-JAN-1995 (first entry)
DT	
XX	
DE	Human mdr-1 promoter fragment.
XX	
XX	inducible promoter; cytostatic agent; adriamycin; vincristine;
KW	multiple drug resistance; mdr-1; mammalian expression vector;
KW	cancer therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	DE4238778-A1.
XX	
PD	19-MAY-1994.
XX	
XX	12-NOV-1992; 92DE-04238778.
PF	
XX	12-NOV-1992; 92DE-04238778.
PR	
XX	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PA	
XX	Stein U, Walther W;
PI	
XX	
DR	WPI; 1994-168680/21.
XX	
XX	New mammalian expression vector useful for gene therapy, - comprising the
PT	promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT	cytostatic agents.
PT	
XX	Claim 2; Page 4; 7pp; German.
PS	
XX	This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC	human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC	cytostatic agents such as vincristine and adriamycin which are used in
CC	cancer therapy. Vectors comprising the promoter and enhancer sequences
CC	operably linked to heterologous genes coding for therapeutic agents are
CC	claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
CC	interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
CC	control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
SQ	Sequence 2090 BP; 714 A; 365 C; 444 G; 567 T; 0 U; 0 Other;
	Query Match 19.4%; Score 30.8; DB 2; Length 2090;
	Best Local Similarity 63.5%; Pred. No. 38;
	Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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DB	112 AGAATCTATTATTAAATCTGTATTCTTGAATCTTAACTTACTTATATCTTTGATAG 171
QY	146 TGATGCTTCTCTGA 159
DB	172 AGATCTTACCCTGA 185
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ID	ADY95063 standard; DNA; 3060 BP.
XX	
AC	ADY95063;
XX	
DT	16-JUN-2005 (first entry)
XX	
XX	Multi-drug resistance 1 (MDR1) gene polynucleotide SEQ ID NO 1.
XX	

Search completed: December 8, 2005, 00:35:17
Job time : 487 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 00:19:41 ; Search time 140 Seconds
(without alignments)

2018.802 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atgagagaagtcacataacct.....tcacgtgatgtctctga 159

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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8: /cgn2_6/ptodata/1/ina/RE-COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	159	100.0	16062	3	US-09-949-016-13181 Sequence 13181, A
4	144.6	90.9	159	3	US-09-949-872B-13 Sequence 13, Appl
5	143	89.9	159	3	US-09-949-872B-9 Sequence 9, Appl
6	83	52.2	315	3	US-09-124-671-26 Sequence 26, Appl
7	34.6	21.8	2071	3	US-09-023-023-1 Sequence 1, Appl
8	33.2	20.9	601	3	US-09-949-016-135505 Sequence 135505, A
9	33.2	20.9	601	3	US-09-949-016-135525 Sequence 135525, A
10	33.2	20.9	75929	3	US-09-949-016-15543 Sequence 15543, A
11	33.2	20.9	75929	3	US-09-949-016-15543 Sequence 15543, A
12	32.2	20.3	3713	2	US-08-100-709-1 Sequence 1, Appl
13	32.2	20.3	3713	2	US-08-176-865-1 Sequence 1, Appl
14	32.2	20.3	3713	2	US-08-474-038-1 Sequence 1, Appl
15	32.2	20.3	3713	2	US-08-779-046-1 Sequence 1, Appl
16	32.2	20.3	3713	2	US-08-881-340-1 Sequence 1, Appl
17	32.2	20.3	59240	3	US-09-949-016-11933 Sequence 11933, A
18	31.8	20.0	1421	3	US-08-956-171B-283 Sequence 283, App
19	31.8	20.0	1421	3	US-08-781-986A-283 Sequence 283, App
20	31.6	19.9	264358	3	US-09-949-016-15725 Sequence 15725, A
21	31.4	19.7	601	3	US-09-949-016-15725 Sequence 15725, A
22	31.4	19.7	601	3	US-09-949-016-26392 Sequence 26392, A
23	31.4	19.7	601	3	US-09-949-016-35374 Sequence 35374, A
24	31.4	19.7	601	3	US-09-949-016-120416 Sequence 120416, A
C 24	31.4	19.7	601	3	US-09-949-016-120420 Sequence 120420, A

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35	30.4	19.1	278866	3	US-09-949-016-13925 Sequence 13925, A
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37	30.4	19.1	278866	3	US-09-949-016-14699 Sequence 14699, A
38	30.4	19.1	278866	3	US-09-949-016-14700 Sequence 14700, A
39	30.4	19.1	278866	3	US-09-949-016-14701 Sequence 14701, A
40	30.4	19.1	278866	3	US-09-949-016-14702 Sequence 14702, A
41	30.4	19.1	278866	3	US-09-949-016-14703 Sequence 14703, A
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46	30.2	19.0	161914	3	US-09-949-016-12906 Sequence 12906, A
C 47	30	18.9	601	3	US-08-998-416-295 Sequence 295, App
C 48	30	18.9	859	3	US-09-949-016-196215 Sequence 196215, A
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51	30	18.9	227390	3	US-09-949-016-12201 Sequence 12201, A
52	30	18.9	227391	3	US-09-949-016-13365 Sequence 13365, A
C 53	29.8	18.7	380	3	US-09-621-976-9957 Sequence 9957, Ap
54	29.8	18.7	972	3	US-09-949-016-2818 Sequence 2818, Ap
55	29.6	18.6	601	3	US-09-949-016-38341 Sequence 38341, A
56	29.6	18.6	601	3	US-09-949-016-38342 Sequence 38342, A
57	29.6	18.6	1539	3	US-09-248-796A-116 Sequence 116, App
58	29.6	18.6	17807	3	US-09-949-016-12779 Sequence 12779, A
59	29.6	18.6	17864	3	US-09-949-016-15511 Sequence 15511, A
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65	29.4	18.5	601	3	US-09-949-016-106210 Sequence 106210, A
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67	29.4	18.5	601	3	US-09-949-016-106608 Sequence 106608, A
68	29.4	18.5	601	3	US-09-949-016-106807 Sequence 106807, A
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72	29.4	18.5	601	3	US-09-949-016-107132 Sequence 107132, A
73	29.4	18.5	601	3	US-09-949-016-107174 Sequence 107174, A
74	29.4	18.5	601	3	US-09-949-016-107216 Sequence 107216, A
75	29.4	18.5	601	3	US-09-949-016-107258 Sequence 107258, A
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77	29.4	18.5	2109	3	US-08-956-171B-416 Sequence 416, App
78	29.4	18.5	2109	3	US-08-781-986A-416 Sequence 416, App
C 79	29.2	18.4	555	3	US-09-621-976-2784 Sequence 2784, App
C 80	29.2	18.4	76563	3	US-09-949-016-17099 Sequence 17099, A
C 81	29.2	18.4	78269	3	US-09-949-016-12497 Sequence 12497, A
C 82	29	18.2	456	3	US-09-248-796A-610 Sequence 610, App
83	29	18.2	48149	3	US-09-949-016-15258 Sequence 15258, A
84	29	18.2	236474	3	US-09-949-016-13418 Sequence 13418, A
85	29	18.2	239527	3	US-09-949-016-15980 Sequence 15980, A
86	29	18.2	300402	3	US-09-949-016-15980 Sequence 15980, A
C 87	28.8	18.1	601	3	US-09-949-016-13632 Sequence 13632, A
C 88	28.8	18.1	1881	3	US-09-949-016-193542 Sequence 193542, A
C 89	28.8	18.1	4084	9	US-08-851-567B-27 Patent No. 5198347-5
C 90	28.8	18.1	5050	3	US-09-949-016-1132 Sequence 132, App
C 91	28.8	18.1	5055	3	US-08-851-567B-25 Sequence 25, Appl
C 92	28.8	18.1	23222	3	US-09-949-016-15949 Sequence 15949, A
C 93	28.8	18.1	25922	3	US-09-949-016-11874 Sequence 11874, A
C 94	28.8	18.1	49416	3	US-09-949-016-15234 Sequence 15234, A
C 95	28.8	18.1	50368	3	US-09-949-016-13256 Sequence 13256, A
C 96	28.8	18.1	105733	3	US-09-949-016-113080 Sequence 13080, A
C 97	28.8	18.1	156324	3	US-09-949-016-13749 Sequence 13749, A

28.8 18.1 268449 3 US-09-949-016-17244 Sequence 17244, A
28.6 18.0 603 3 US-09-543-681A-2490 Sequence 2490, Ap
28.6 18.0 2533 3 US-10-104-047-130 Sequence 130, App
ALIGNMENTS
RESULT 1
US-09-513-999C-10799
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799
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Best Local Similarity 100.0%; Pred. No. 2.3e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 60
Db 196 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 255
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db 256 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 315
QY 121 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 159
Db 316 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 354
RESULT 2
US-09-949-016-1439
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439

Query Match 100.0%; Score 159; DB 3; Length 1635;
Best Local Similarity 100.0%; Pred. No. 3.4e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 60
Db 182 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 241
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db 242 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 340
RESULT 3
US-09-949-016-13181
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181
Query Match 100.0%; Score 159; DB 3; Length 16062;
Best Local Similarity 100.0%; Pred. No. 7e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 60
Db 12608 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCCCTCAACCAATTGAAATG 12667
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db 12668 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 12727
QY 121 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 159
Db 12728 TGTCTCTTGTGATCTGATATCATCGTGATGCTTCTCTGA 12766
RESULT 4
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15

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; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9112736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PLB cDNA
US-09-549-872B-13

Query Match          90.9%; Score 144.6; DB 3; Length 159;
Best Local Similarity 94.3%; Pred. No. 5.4e-36;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTATAGAGAGCTCAACCATTTGAAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTGCTATAGAGAGCTTCAACCATTTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTTCAAGACCTATTTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGCTCTTCTGCTGCTGCTATCATGCTGATGCTTCTCTGA 159
DB 121 TGCTCTTCTGCTGCTGCTATCATGCTGATGCTTCTCTGA 159

RESULT 5
US-09-549-872B-9
; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9

Query Match          89.9%; Score 143; DB 3; Length 159;
Best Local Similarity 93.7%; Pred. No. 1.7e-35;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTATAGAGAGCTTCAACCATTTGAAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTGCTATAGAGAGCTTCAACCATTTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTTCAAGACCTATTTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGCTCTTCTGCTGCTGCTATCATGCTGATGCTTCTCTGA 159
DB 121 TGCTCTTCTGCTGCTGCTATCATGCTGATGCTTCTCTGA 159

RESULT 6
US-09-124-671-26
; Sequence 26, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-09-124-671-26

Query Match          52.2%; Score 83; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGTA 133
DB 98 GTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGTA 157
QY 134 TCTGTATCATCGTGATGCTTCTC 156
DB 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 7
US-09-023-023-1
; Sequence 1, Application US/09023023
; Patent No. 6121018
; GENERAL INFORMATION:
; APPLICANT: Kristine Kay Kikly
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Pr
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,023
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,030
; FILING DATE: March 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GHS0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2071 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-023-023-1

Query Match      21.8%; Score 34.6; DB 3; Length 2071;
Best Local Similarity 58.1%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 44;

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Db 1215 ATCAGAGAAATTCACCATTTATCAGCTTCAAGAGCATTTTATCAGCAGCATCCA 1274

QY 94 TTATCAATTTCTGCTCATCTTAATATGCTCTCTTGGCTGATCTG 138
Db 1275 TGTTAAACCTTTGCTCTTTCATTTAAAGTGAAACATATGAACTGT 1319

RESULT 8
US-09-949-016-135505
; Sequence 135505, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135505
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135505

Query Match      20.9%; Score 33.2; DB 3; Length 601;
Best Local Similarity 54.0%; Pred. No. 0.8;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 115 CTCAGCCTTCCAAAGTGCCGGGATCAGCGGTGAACCAACCGCCGACCAAGTTCT 174

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGATCATCGT 146
Db 175 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTAAGTTAATGAGCAGTGCTATTGT 234

QY 147 GATGCT 152
Db 235 AGTGCT 240

RESULT 9
US-09-949-016-135525
; Sequence 135525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135505
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135505

Query Match      20.9%; Score 33.2; DB 3; Length 601;
Best Local Similarity 54.0%; Pred. No. 0.8;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 115 CTCAGCCTTCCAAAGTGCCGGGATCAGCGGTGAACCAACCGCCGACCAAGTTCT 174

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGATCATCGT 146
Db 175 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTAAGTTAATGAGCAGTGCTATTGT 234

QY 147 GATGCT 152
Db 235 AGTGCT 240

RESULT 9
US-09-949-016-135525
; Sequence 135525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135505
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135525

Query Match      20.9%; Score 33.2; DB 3; Length 75929;
Best Local Similarity 54.0%; Pred. No. 3.7;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 31048 CTCAGCCTTCCAAAGTGCCGGGATCAGCGGTGAACCAACCGCCGACCAAGTTCT 31107

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGATCATCGT 146
Db 31108 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTAAGTTAATGAGCAGTGCTATTGT 31167

QY 147 GATGCT 152
```

Db 31168 AGTGCT 31173

|||||

RESULT 11

US-09-949-016-15544

; Sequence 15544, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIORITY FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15544

; LENGTH: 75929

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(75929)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15544

Query Match 20.9%; Score 33.2; DB 3; Length 75929;

Best Local Similarity 54.0%; Pred. No. 3.7;

Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAGACGCTCAACATTGAATGCCTCAAGCAGCAGTCAAAAGCTACA 86

Db 31048 CTCAGCTCCCAAGTTCGGGATCACAGCGTGAACCCAGCCGACCAACAGTTCT 31107

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGATCATCGT 146

Db 31108 TTTTATATATTCAGCTCTTCTCTATTAATAAACTTTAAGTTAATGAGCAGTCTATTGT 31167

QY 147 GATGCT 152

Db 31168 AGTGCT 31173

|||||

RESULT 12

US-08-100-709-1/c

; Sequence 1, Application US/08100709

; Patent No. 5322687

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yuping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,865

FILING DATE: 30-DEC-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,709

FILING DATE: 19930729

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3713 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 99..3602

US-08-100-709-1

Query Match 20.3%; Score 32.2; DB 2; Length 3713;

Best Local Similarity 61.2%; Pred. No. 2.9;

Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTG 132

Db 441 CTTAAATGCTTCAGCGTATATTGATTAATTTCTCCCTAATCTCTTAATTCAGTGATTG 382

QY 133 ATCTGATCATCGTGATGCTTCTCT 157

Db 381 CTTTGTCTTACTGTTGCTTCTAT 357

|||||

RESULT 13

US-08-176-865-1/c

; Sequence 1, Application US/08176865

; Patent No. 5616319

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yuping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,865

FILING DATE: 30-DEC-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

COMPUTER: IBM PC compatible

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-176-865-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATAATGCTCTTGTGCTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATCCTTCTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357

RESULT 14
US-08-474-038-1/c
; Sequence 1, Application US/08474038
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular

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; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-474-038-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATAATGCTCTTGTGCTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATCCTTCTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357

RESULT 15
US-08-779-046-1/c
; Sequence 1, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-779-046-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Qy 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGTTCTTGTGCTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTGATAATTTCTCCCTAATCCTTCTAATTCAGTGATTG 382
Qy 133 ATCTGTATCATCGTGTATGTTCTTCT 157
Db 381 CTTTGTCTTACTGTGTTGTTCTAT 357

RESULT 16

US-08-881-340-1/c
; Sequence 1, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-881-340-1

Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGTTCTTGTGCTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTGATAATTTCTCCCTAATCCTTCTAATTCAGTGATTG 382
Qy 133 ATCTGTATCATCGTGTATGTTCTTCT 157
Db 381 CTTTGTCTTACTGTGTTGTTCTAT 357

RESULT 17

US-09-949-016-11933/c
; Sequence 11933, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11933
; LENGTH: 59240
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11933

Query Match 20.3%; Score 32.2; DB 3; Length 59240;
Best Local Similarity 59.1%; Pred. No. 7;
Matches 55; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 19 CTCACCTGCTCAGCTATAAGAAGAGCTCAACCACTTGAATGCTCAACAGCAGCTCAA 78
Db 49395 CTCCTTCACACACCTACTACTAATCAGATCCACATTTAAATGATCCCGAGTGATTCT 49336
Qy 79 AGCTACAGAATCTATTATCAATTTCTGTCTC 111
Db 49335 AGCTATTAAAGATATTGTAAAGTTCTATTTC 49303

RESULT 18

US-08-956-171E-283
; Sequence 283, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hymen

```

;
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 283:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1421 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-08-956-171E-283

Query Match      20.0%; Score 31.8; DB 3; Length 1421;
Best Local Similarity 61.4%; Pred. No. 2.9;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 36 AAGAAGAGCCTCAACCATTTGAATGCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATT 95
Db 317 ACGAAGAAACTGAAATTTTGAATGGGTGATATCATGTCAAAATATAGTCAAGATGTA 376

QY 96 TATCAATTTCTGCTCATCTTAA 118
Db 377 CTTCAATTACTCTATAAAATAA 399

RESULT 20
US-09-949-016-15725/c
; Sequence 15725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15725
; LENGTH: 264358
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(264358)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15725

Query Match      19.9%; Score 31.6; DB 3; Length 264358;
Best Local Similarity 53.2%; Pred. No. 17;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 16 TACCTCAGTCGCTCAGCTATAGAAGAGCCTCAACCATTTGAATGCTCAACAAGCAGCT 75
Db 104340 TACCTTTCTTCCATCTCGGCTGAGTAAACCTGCCATTCCTTCATGATTAAAGAGG 104281

QY 76 CAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTCTTGTCTGATC 135
Db 104280 CAGAAACCTCAGAAATATTTTCTTATTTCTGTCTCATCTTGAATACC 104221

QY 136 TGTATC 141
Db 104220 AGTTTC 104215

RESULT 21
US-09-949-016-26392/c
; Sequence 26392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

```

```

;
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 283:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1421 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-08-956-171E-283

Query Match      20.0%; Score 31.8; DB 3; Length 1421;
Best Local Similarity 61.4%; Pred. No. 2.9;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 36 AAGAAGAGCCTCAACCATTTGAATGCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATT 95
Db 317 ACGAAGAAACTGAAATTTTGAATGGGTGATATCATGTCAAAATATAGTCAAGATGTA 376

QY 96 TATCAATTTCTGCTCATCTTAA 118
Db 377 CTTCAATTACTCTATAAAATAA 399

RESULT 19
US-08-781-986A-283
; Sequence 283, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-283

Query Match      20.0%; Score 31.8; DB 3; Length 1421;
Best Local Similarity 61.4%; Pred. No. 2.9;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26392
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26392

Query Match      19.7%; Score 31.4; DB 3; Length 601;
Best Local Similarity 56.6%; Pred. No. 2.9;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTGTTATGTGMAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 22
US-09-949-016-35374/c
; Sequence 35374, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35374
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35374

Query Match      19.7%; Score 31.4; DB 3; Length 601;
Best Local Similarity 56.6%; Pred. No. 2.9;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTGTTATGTGMAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 23
US-09-949-016-120416/c
; Sequence 120416, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120416
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-120416/c

Query Match      19.7%; Score 31.4; DB 3; Length 601;
Best Local Similarity 56.6%; Pred. No. 2.9;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTGTTATGTGMAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 24
US-09-949-016-120420/c
; Sequence 120420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120420
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-120420

Query Match      19.7%; Score 31.4; DB 3; Length 601;
Best Local Similarity 56.6%; Pred. No. 2.9;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTGTTATGTGMAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 25
US-08-439-814-1
; Sequence 1, Application US/08439814
; Patent No. 5968735
; GENERAL INFORMATION:
; APPLICANT: STEIN, Urike
; APPLICANT: WALTHER, Wolfgang
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
; TITLE OF INVENTION: THERAPY-RELEVANT GENES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIKO, MARMELSTEIN, MURRAY & ORAM LLP
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14706
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14706

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

Qy 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
Db 40407 TTGTTTATACCTCTTTTATCCATTCATATTGAT 40442

RESULT 29
US-09-949-016-14707
; Sequence 14707, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14707
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14707

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

Qy 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
Db 40407 TTGTTTATACCTCTTTTATCCATTCATATTGAT 40442

RESULT 30
US-09-949-016-14708
; Sequence 14708, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14708
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14708

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

Qy 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
Db 40407 TTGTTTATACCTCTTTTATCCATTCATATTGAT 40442

RESULT 31
US-09-949-016-14709
; Sequence 14709, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14709
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14709

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

Qy 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
Db 40407 TTGTTTATACCTCTTTTATCCATTCATATTGAT 40442

RESULT 32
US-09-949-016-13922
; Sequence 13922, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13922
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13922

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCTCTGCTGCTATCATCGTAT 149
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTCTGCTGCTATCATCGTAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

RESULT 33
US-09-949-016-13923
Sequence 13923, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13923
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13923

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCTCTGCTGCTATCATCGTAT 149
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTCTGCTGCTATCATCGTAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13924
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13924

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCTCTGCTGCTATCATCGTAT 113
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTCTGCTGCTATCATCGTAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

RESULT 35
US-09-949-016-13925
Sequence 13925, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13925
LENGTH: 278866
TYPE: DNA
ORGANISM: Human

FEATURE: ;
NAME/KEY: misc_feature ;
LOCATION: (1)...(278866) ;
OTHER INFORMATION: n = A,T,C or G ;
US-09-949-016-13925

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211
QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 36
US-09-949-016-13926
Sequence 13926, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13926
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13926

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211
QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 37
US-09-949-016-14699
Sequence 14699, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14699
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14699
Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211
QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 38
US-09-949-016-14700
Sequence 14700, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14700
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14700

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211
QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 39

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US-09-949-016-14701
; Sequence 14701, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14701
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14701

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCCCTCTTTATCCATTCATATGAT 264247

RESULT 40
US-09-949-016-14702
; Sequence 14702, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14702
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCCCTCTTTATCCATTCATATGAT 264247

RESULT 40
US-09-949-016-14702
; Sequence 14702, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14702
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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QY 54 TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCCCTCTTTATCCATTCATATGAT 264247

RESULT 41
US-09-949-016-14703
; Sequence 14703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14703
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14703

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 264152 TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCCCTCTTTATCCATTCATATGAT 264247

RESULT 42
US-09-949-016-15088
; Sequence 15088, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15088
; LENGTH: 9811

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15088

Query Match      19.0%; Score 30.2; DB 3; Length 9811;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATGGAATGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4316 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 4375

QY 87 GAATCTATTATCAATTTCTCTCATCTTAAATATGCT 125
DB 4376 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTT 4414

RESULT 43
US-09-949-016-15089
; Sequence 15089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15089
; LENGTH: 9811
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15089

Query Match      19.0%; Score 30.2; DB 3; Length 9811;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATGGAATGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4316 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 4375

QY 87 GAATCTATTATCAATTTCTCTCATCTTAAATATGCT 125
DB 4376 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTT 4414

RESULT 44
US-09-949-016-12176
; Sequence 12176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12176
; LENGTH: 9864
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12176

Query Match      19.0%; Score 30.2; DB 3; Length 9964;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATGGAATGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4472 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAATCTATCTTGTGAAAGTCTATA 4531

QY 87 GAATCTATTATCAATTTCTCTCATCTTAAATATGCT 125
DB 4532 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTT 4570

RESULT 45
US-09-949-016-12685
; Sequence 12685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12685
; LENGTH: 16190
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12685

Query Match      19.0%; Score 30.2; DB 3; Length 16190;
Best Local Similarity 60.2%; Pred. No. 41;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 23 CTCGCTCAGCTATAAGAGAGCGCTCAACCAATGGAATGCTCAACAGCAGCTCAAAAGC 82
DB 161769 CTCTCTTGGCATCTGCTCAGCTAAACCAATGAATGGCTTTACATCAGACTAAACA 161828

QY 83 TACAGATCTATTATCAATTTC 105
DB 161829 AACAAACACTTTGTAGGTATATC 161851

RESULT 46
US-09-949-016-12906
; Sequence 12906, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12906
; LENGTH: 161914
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(161914)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12906

Query Match 19.0%; Score 30.2; DB 3; Length 161914;
Best Local Similarity 60.2%; Pred. No. 41;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 23 CTCGCTCAGCTATAGAAAGCGCTCAACCAATGCTCAACCAAGCAGTCAAAAGC 82
Db 161779 CTCCTCTGCCATCTCTCAGCGCTCAACCAATGCTTACCAATCAGACTAAACA 161838

QY 83 TACAGAACTATTATCAATTC 105
Db 161839 AACAACTTTGTAGGTATATC 161861

RESULT 47
US-09-949-016-196215/c
; Sequence 196215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196215
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-196215

Query Match 18.9%; Score 30; DB 3; Length 601;
Best Local Similarity 52.4%; Pred. No. 8;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 23 CTCGCTCAGCTATAGAAAGCGCTCAACCAATGCTCAACCAAGCAGTCAAAAGC 82
Db 446 CTGCTCAGCTCTCTGATAGCTGGACTATATGACACCAACCATGCTGGCTAATTA 387

QY 83 TACAGAACTATTATCAATTC 105
Db 386 CTTTATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 327

QY 143 TCGTGA 148

Db 326 TTTTGA 321

RESULT 48
US-08-998-416-295/c
; Sequence 295, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 295:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1244UP
; US-08-998-416-295

Query Match 18.9%; Score 30; DB 3; Length 859;
Best Local Similarity 53.4%; Pred. No. 9;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 16 TACCTCAGCTCAGCTATAGAAAGCGCTCAACCAATGCTCAACCAAGCAGT 75
Db 489 TGCTTAAATGGTCCACGAGCATGAGTGGCCGCTGTTGATATATACATATATGGGATT 430

QY 76 CAAAAGCTACAGATCTATTATTAATTCATCTCTCATCTTAATATCTCTTCTGCTGA 133
Db 429 CATACGCAACTGAAGCTAGTTCGAAGTTGGCTCTCTCTTATATCTTACTTAGGAGA 372

RESULT 49
US-09-949-016-12542
; Sequence 12542, Application US/09949016
; Patent No. 6812339


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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12542
; LENGTH: 173787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12542

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```

Query Match      18.9%; Score 30; DB 3; Length 173787;
Best Local Similarity 52.4%; Pred. No. 48;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy      23 CTCGCTCAGCTATAGAGAGCCTCAACCAATGAAATGCTCAACAGCAGTCACAAAGC 82
Db      72869 CTGCTCAGCTCTCTGAATAGCTGGACTATATATGACACACCATGCGCTGGCTAATTA 72928

Qy      83 TACAGATCTATTATCAATTTCTGTCATCTTAATATGTCCTGCTGATCTGTATCA 142
Db      72929 CTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 72988

Qy      143 TCGTGA 148
Db      72989 TTTTGA 72994

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RESULT 50
US-09-949-016-17302
; Sequence 17302, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17302
; LENGTH: 173791
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17302

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Query Match      18.9%; Score 30; DB 3; Length 173791;
Best Local Similarity 52.4%; Pred. No. 48;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy      23 CTCGCTCAGCTATAGAGAGCCTCAACCAATGAAATGCTCAACAGCAGTCACAAAGC 82
Db      72869 CTGCTCAGCTCTCTGAATAGCTGGACTATATATGACACACCATGCGCTGGCTAATTA 72928

Qy      83 TACAGATCTATTATCAATTTCTGTCATCTTAATATGTCCTGCTGATCTGTATCA 142

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Db      72929 CTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 72988

Qy      143 TCGTGA 148
Db      72989 TTTTGA 72994

Search completed: December 8, 2005, 02:16:30
Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 01:11:35 ; Search time 809 Seconds

(without alignments)
1625.255 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atggagaaagtcacact.....tcacgtgatgtctctga 159

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	159	100.0	525	3	US-09-918-995-4045
3	159	100.0	1635	3	US-09-873-367C-162
4	159	100.0	1635	9	US-10-843-641A-162
5	159	100.0	1712	10	US-11-019-855-1
6	158	99.4	380	3	US-09-918-995-3950
7	158	99.4	418	3	US-09-918-995-5235
8	157.4	99.0	334	3	US-09-918-995-4217
9	147.8	93.0	487	3	US-09-918-995-5377
10	147.8	93.0	492	3	US-09-918-995-17377
11	144.6	90.9	159	6	US-10-371-101-13
12	144.6	90.9	407	3	US-09-918-995-3842
13	143	89.9	159	6	US-10-371-101-9
14	83	52.2	315	8	US-10-815-514-26
15	83	52.2	315	8	US-10-877-930-26
16	83	52.2	315	9	US-10-873-594-26
17	46	28.9	108	8	US-10-724-532-3
18	46	28.9	108	8	US-10-724-532-4
19	46	28.9	135	8	US-10-724-532-5
20	46	28.9	135	8	US-10-724-532-6
21	34.2	21.5	589	4	US-09-925-065A-575150
22	34.2	21.5	589	4	US-09-925-065A-575151
23	34.2	21.5	786452	8	US-10-719-993-6822

C 24	33.4	21.0	37973	6	US-10-311-455-2169	Sequence 2169, Ap
C 25	33.2	20.9	201	8	US-10-719-993-26457	Sequence 26457, A
C 26	32.6	20.5	170279	8	US-10-388-938-1	Sequence 1, Appli
C 27	32.2	20.3	402	10	US-11-029-984-845	Sequence 845, App
C 28	32	20.1	451	4	US-09-925-065A-150093	Sequence 150093, App
C 29	31.8	20.0	359	5	US-10-027-632-140279	Sequence 140279, App
C 30	31.8	20.0	359	6	US-10-027-632-140279	Sequence 140279, App
C 31	31.8	20.0	636	4	US-09-925-065A-536994	Sequence 536994, App
C 32	31.8	20.0	1421	2	US-08-781-986A-283	Sequence 283, App
C 33	31.8	20.0	1421	7	US-10-329-624-283	Sequence 283, App
C 34	31.8	20.0	6025	8	US-10-857-625-76	Sequence 76, Appl
C 35	31.6	19.9	812	4	US-09-925-065A-179738	Sequence 179738, App
C 36	31.4	19.7	519	4	US-09-925-065A-255686	Sequence 255686, App
C 37	31.4	19.7	519	4	US-09-925-065A-255687	Sequence 255687, App
C 38	31.4	19.7	560	4	US-09-925-065A-246839	Sequence 246839, App
C 39	31.4	19.7	873	9	US-10-450-763-5048	Sequence 5048, App
C 40	31.4	19.7	873	9	US-10-450-763-5355	Sequence 5355, App
C 41	31.4	19.7	873	9	US-10-450-763-11273	Sequence 11273, A
C 42	31.4	19.7	1199	7	US-10-437-963-88801	Sequence 88801, A
C 43	31.4	19.7	3505	10	US-11-097-143-27115	Sequence 27115, A
C 44	31.4	19.7	5875	6	US-10-311-455-261	Sequence 261, App
C 45	31.4	19.7	2940917	5	US-10-027-632-174763	Sequence 174763, App
C 46	31.4	19.7	2940917	6	US-10-027-632-174763	Sequence 174763, App
C 47	31.2	19.6	453	7	US-10-424-599-49155	Sequence 49155, A
C 48	31.2	19.6	84073	5	US-10-087-192-712	Sequence 712, App
C 49	31	19.5	633	5	US-10-027-632-233567	Sequence 233567, App
C 50	31	19.5	633	6	US-10-027-632-233567	Sequence 233567, App
C 51	31	19.5	663	8	US-10-425-115-47211	Sequence 47211, A
C 52	31	19.5	1269	8	US-10-767-795-1475	Sequence 1475, App
C 53	31	19.5	2162	7	US-10-437-963-18523	Sequence 18523, A
C 54	31	19.5	5206	7	US-10-437-963-77914	Sequence 77914, A
C 55	31	19.5	6182	6	US-10-311-455-1988	Sequence 87, Appl
C 56	31	19.5	271990	6	US-10-195-144-87	Sequence 87, Appl
C 57	31	19.5	271990	6	US-10-345-072-87	Sequence 264616, App
C 58	30.8	19.4	309	5	US-10-027-632-264616	Sequence 264616, App
C 59	30.8	19.4	309	5	US-10-027-632-264617	Sequence 264617, App
C 60	30.8	19.4	309	6	US-10-027-632-264616	Sequence 264617, App
C 61	30.8	19.4	309	6	US-10-027-632-264617	Sequence 264617, App
C 62	30.8	19.4	437	8	US-10-767-795-1993	Sequence 1993, App
C 63	30.8	19.4	524	4	US-09-925-065A-418006	Sequence 418006, App
C 64	30.8	19.4	739	4	US-09-925-065A-85147	Sequence 85147, A
C 65	30.8	19.4	10200	9	US-10-415-607-5	Sequence 5, Appli
C 66	30.8	19.4	177380	8	US-10-484-577-683	Sequence 683, App
C 67	30.6	19.2	336	4	US-09-925-065A-143336	Sequence 143336, App
C 68	30.6	19.2	349	3	US-09-960-352-1428	Sequence 1428, Ap
C 69	30.6	19.2	426	8	US-10-674-124A-2911	Sequence 2911, Ap
C 70	30.6	19.2	442	4	US-09-925-065A-644502	Sequence 644502, A
C 71	30.6	19.2	496	3	US-09-918-995-25194	Sequence 25194, A
C 72	30.6	19.2	541	4	US-09-925-065A-216894	Sequence 216894, A
C 73	30.6	19.2	551	3	US-09-867-701-6051	Sequence 6051, Ap
C 74	30.6	19.2	596	4	US-09-925-065A-302480	Sequence 302480, App
C 75	30.6	19.2	607	4	US-09-925-065A-655605	Sequence 655605, App
C 76	30.6	19.2	930	7	US-10-220-120-9	Sequence 9, Appli
C 77	30.6	19.2	1132	5	US-10-103-313-67	Sequence 67, Appl
C 78	30.6	19.2	1192	9	US-10-756-149-180	Sequence 180, App
C 79	30.6	19.2	1973	3	US-09-814-353-20163	Sequence 20163, A
C 80	30.6	19.2	89873	9	US-10-461-862-61	Sequence 61, Appl
C 81	30.6	19.2	95109	7	US-10-433-287-80	Sequence 80, Appl
C 82	30.4	19.1	542	4	US-09-925-065A-828136	Sequence 828136, App
C 83	30.4	19.1	561	4	US-09-925-065A-828135	Sequence 828135, App
C 84	30.4	19.1	563	4	US-09-925-065A-828135	Sequence 828135, App
C 85	30.4	19.1	570	4	US-09-925-065A-828142	Sequence 828142, App
C 86	30.4	19.1	604	4	US-09-925-065A-832584	Sequence 832584, App
C 87	30.4	19.1	614	4	US-09-925-065A-750309	Sequence 750309, App
C 88	30.4	19.1	614	4	US-09-925-065A-750310	Sequence 750310, App
C 89	30.4	19.1	614	4	US-09-925-065A-822696	Sequence 822696, App
C 90	30.2	19.0	248	8	US-10-674-124A-8992	Sequence 8992, Ap
C 91	30.2	19.0	277	3	US-09-294-093B-2256	Sequence 2256, Ap
C 92	30.2	19.0	433	5	US-10-027-632-140644	Sequence 140644, App
C 93	30.2	19.0	433	5	US-10-027-632-140645	Sequence 140645, App
C 94	30.2	19.0	433	6	US-10-027-632-140645	Sequence 140645, App
C 95	30.2	19.0	433	6	US-10-027-632-140645	Sequence 140645, App
C 96	30.2	19.0	565	4	US-09-925-065A-803161	Sequence 803161, App

QY 1 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
Sequence 100666, 60
Db 310 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 369
Sequence 100666, 369
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Sequence 129555, 120
Db 370 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 429
Sequence 129555, 429
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
Sequence 159, 159
Db 430 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 468
Sequence 159, 468
RESULT 3
US-09-873-367C-162
; Sequence 162, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162
Query Match 100.0%; Score 159; DB 3; Length 1635;
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
Db 182 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 241
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 242 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 340
RESULT 4
US-10-843-641A-162
; Sequence 162, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; APPLICANT: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A

Sequence 6502, Ap
Sequence 100666, 60
Sequence 100666, 369
Sequence 129555, 120
Sequence 129555, 429
ALIGNMENTS
US-10-691-412-1
; Sequence 1, Application US/10691412
; Publication No. US20040191802A1
; GENERAL INFORMATION:
; APPLICANT: Kranias, Evangelia G.
; APPLICANT: Kobra, Haghighi
; TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
; FILE REFERENCE: 10738-47
; CURRENT APPLICATION NUMBER: US/10/691,412
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1
Query Match 100.0%; Score 159; DB 8; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
Db 1 ATGGAGAAAGTCCAATACCTCAGTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
Db 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
RESULT 2
US-09-918-995-4045
; Sequence 4045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4045
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(525)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4045
Query Match 100.0%; Score 159; DB 3; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.6e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-162

Query Match      100.0%; Score 159; DB 9; Length 1635;
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 60
Db      182 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 241

QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db      242 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 301

QY      121 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 159
Db      302 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 340

RESULT 6
US-09-918-995-3950
; Sequence 3950, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3950
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(380)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-3950

Query Match      99.4%; Score 158; DB 3; Length 380;
Best Local Similarity 99.4%; Pred. No. 4.5e-37;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 60
Db      182 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 241

QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db      242 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 301

QY      121 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 159
Db      302 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 340

RESULT 7
US-09-918-995-5235
; Sequence 5235, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5235
; LENGTH: 418
; TYPE: DNA

QY      1  ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 60
Db      182 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATATAAGAGAGCCTCAACCATTTGAAATG 241

QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
Db      242 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 301

QY      121 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 159
Db      302 TGTCTCTTGTGATCTGTATCATCGTGAATGCTTCTCTGA 340

US-11-019-855-1
; Sequence 1, Application US/11019855
; Publication No. US20050158771A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: novel targets for obesity from skeletal muscle
; FILE REFERENCE: case 22314
; CURRENT APPLICATION NUMBER: US/11/019,855
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: phospholamban (PLN)
; LOCATION: (1)-(1712)
; OTHER INFORMATION: accession No.s: NM002667.2; Hs.85050; LocusID: 5350
US-11-019-855-1

Query Match      100.0%; Score 159; DB 10; Length 1712;
Best Local Similarity 100.0%; Pred. No. 4.3e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(418)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5235

Query Match      99.4%; Score 158; DB 3; Length 418;
Best Local Similarity 99.4%; Pred. No. 4.7e-37;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
Db 156 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 215

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 120
Db 216 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 275

QY 121 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 159
Db 276 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 314

RESULT 8
US-09-918-995-4217
; Sequence 4217, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4217
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4217

Query Match      99.0%; Score 157.4; DB 3; Length 394;
Best Local Similarity 99.4%; Pred. No. 7e-37;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
Db 182 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 241

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 120
Db 242 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 301

QY 121 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 340

RESULT 9
US-09-918-995-5377
; Sequence 5377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5377
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5377

Query Match      93.0%; Score 147.8; DB 3; Length 487;
Best Local Similarity 95.6%; Pred. No. 5.8e-34;
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
Db 252 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 311

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 120
Db 312 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 371

QY 121 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 159
Db 372 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 410

RESULT 10
US-09-918-995-17377
; Sequence 17377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17377
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(492)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17377

Query Match      93.0%; Score 147.8; DB 3; Length 492;
Best Local Similarity 95.6%; Pred. No. 5.8e-34;
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
Db 278 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 337

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCATCTTAATA 120
Db 338 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATTAACAATTTCTGTCTCAACTTAA 397

QY 121 TGTCTCTTGTGATCTGTATCATCTGATCGTCTCTCTGA 159
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Db 398 TGTCTCTTGTGATCTGTATCATCTGTGAAGCTTCTTTGA 436

RESULT 11

US-10-371-101-13
; Sequence 13, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PLB cdNA
US-10-371-101-13

Query Match 90.9%; Score 144.6; DB 6; Length 159;
Best Local Similarity 94.3%; Pred. No. 3.3e-33;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCTGTGATGCTTCTCTGA 159
DB 121 TGCCTCTTGTGATTTGCATCATCTGTGATGCTTCTCTGA 159

RESULT 12

US-09-918-995-3842
; Sequence 3842, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3842
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-3842

Query Match 90.9%; Score 144.6; DB 3; Length 407;
Best Local Similarity 94.3%; Pred. No. 4.9e-33;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
DB 182 ATGGAGAAAGTACAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 241
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120
DB 242 CCTCAGGAGCAGCTCAAAAGCTACAGATCTATGTATGAATTTCTGTCTCATCTTAATA 301
QY 121 TGTCTCTTGTGATCTGTATCATCTGTGATGCTTCTCTGA 159
DB 302 TGTCACTTGTGATCTGTATCATCTGTGATGCTTCTCTGA 340
RESULT 13
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Query Match 89.9%; Score 143; DB 6; Length 159;
Best Local Similarity 93.7%; Pred. No. 9.9e-33;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCTGTGATGCTTCTCTGA 159
DB 121 TGCCTCTTGTGATTTGCATCATCTGTGATGCTTCTCTGA 159

RESULT 14

US-10-815-514-26
; Sequence 26, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514

```

; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-815-514-26

Query Match      52.2%; Score 83; DB 8; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 15
US-10-877-930-26
; Sequence 26, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-877-930-26

Query Match      52.2%; Score 83; DB 8; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 16
US-10-873-594-26
; Sequence 26, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-I 065360.0152
US-10-873-594-26

Query Match      52.2%; Score 83; DB 9; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATATGTCCTTGGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 17
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Query Match      28.9%; Score 46; DB 8; Length 108;
Best Local Similarity 65.7%; Pred. No. 0.001; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 35;

QY 54 TGAATGCTCTCAACAGCAGCGTCAAAAGCTACAGAACTCTTAATATGTCCTTGGCTCAT 113
Db 6 TGAGAGAGGCGCTCAGGCCAGGAGAACTCCAGAACTGCTTTTCATGCTTTTGTCTGAT 65

QY 114 CTTAATATGTCCTTGTGTCATCTGTCATCATCGTGATGCTTCT 155
Db 66 TCTCATCTGCTCTCTGCTGATTTGTCATTTATCGTGATGCTCTCT 107

RESULT 18
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: Reticulum
```



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; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match      28.9%; Score 46; DB 8; Length 108;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 103 TGAGAGAGGCTCTCAGGCCAGGACCTCCAGAACTCTTTCATTTGTTGCTCAT 44

QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 43 TCTCATCTGCTCTGCTGCTGATTTGCAATTAATGTCATGCTCT 2

RESULT 19
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match      28.9%; Score 46; DB 8; Length 135;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 18 TGAGAGAGGCTCTCAGGCCAGGACCTCCAGAACTCTTTCATTTGTTGCTCAT 77

QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 78 TCTCATCTGCTCTGCTGCTGATTTGCAATTAATGTCATGCTCT 119

RESULT 20
US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
```

```
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6
```

```
Query Match      28.9%; Score 46; DB 8; Length 135;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 118 TGAGAGAGGCTCTCAGGCCAGGACCTCCAGAACTCTTTCATTTGTTGCTCAT 59

QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 58 TCTCATCTGCTCTGCTGATTTGCAATTAATGTCATGCTCT 17
```

```
RESULT 21
US-09-925-065A-575150/c
; Sequence 575150, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 575150
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-575150
```

```
Query Match      21.5%; Score 34.2; DB 4; Length 589;
Best Local Similarity 52.4%; Pred. No. 7;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

```
QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
DB 284 AAGGAAAAGACTAATAATACATTGAATTCCTCCWATATTTTGAATACTGTTTAAACATTGAACAA 225

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATTTAATA 120
DB 224 CAACAACAATAATCCCAATATACATCTTCACTCTTCCATTATAGAAAATTTAAAG 165

QY 121 TGTCTCTTGTGCTGATCTGATCAT 143
DB 164 TAATCAAACTAATCCATGAAT 142
```

```
RESULT 22
US-09-925-065A-575151/c
; Sequence 575151, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

Db 640785 CAACACAAATCCCAATATACATCTTCTCCATTTATAGAAAATTTAAAG 640726

Qy 121 TGTCTCTTGTGATCTGTATCAT 143

Db 640725 TAATCAAACTTAATCCATAGAAT 640703

RESULT 24

US-10-311-455-2169/c

; Sequence 2169, Application US/10311455

; Publication No. US20030143606A1

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

; APPLICANT: PIEPENBROCK, Christian

; APPLICANT: BERLIN, Kurt

; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation Status of Cytosine Residues

; TITLE OF INVENTION: cytosine methylation

; FILE REFERENCE: 5013.1014

; CURRENT APPLICATION NUMBER: US/10/311,455

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: PCT/EP01/07537

; PRIOR FILING DATE: 2001-07-02

; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: DE 10043826.1

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 2424

; SEQ ID NO 2169

; LENGTH: 37973

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-2169

Query Match 21.0%; Score 33.4; DB 6; Length 37973;

Best Local Similarity 62.7%; Pred. No. 68;

Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 72 ACCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATATGCTCTTGCT 131

Db 12130 ACTTCACATTTATAAATATATTTATCTATAATTTCTTTCTTATAATATCTTTCTCT 12071

Qy 132 GATCTGTATCATCGTGATCGTTC 154

Db 12070 AATTTTAAACAACAAATAATAC 12048

RESULT 25

US-10-719-993-26457/c

; Sequence 26457, Application US/10719993

; Publication No. US20040265849A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001496

; CURRENT APPLICATION NUMBER: US/10/719,993

; CURRENT FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 55342

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26457

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-719-993-26457

Query Match 20.9%; Score 33.2; DB 8; Length 201;

Best Local Similarity 55.1%; Pred. No. 8.9;

Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTCCCAATCACTCGTCTAGCTATAAGAGAGCTCAACATTGAATG 60

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 575151

; LENGTH: 589

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-575151

Query Match 21.5%; Score 34.2; DB 4; Length 589;

Best Local Similarity 52.4%; Pred. No. 7;

Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCCAATCACTCGTCTAGCTATAAGAGAGCTCAACATTGAATG 60

Db 284 AAGGAAAAAGACTAATACATGAATTTTGAATACCTGTTAACATTTGAACAA 225

Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATA 120

Db 224 CAACAACAAATCCCAATATACATCTTCACTCTTCATTTATAGAAAATTTAAAG 165

Qy 121 TGTCTCTTGTGATCTGTATCAT 143

Db 164 TAATCAAACTTAATCCATAGAAT 142

RESULT 23

US-10-719-993-6822/c

; Sequence 6822, Application US/10719993

; Publication No. US20040265849A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001496

; CURRENT APPLICATION NUMBER: US/10/719,993

; CURRENT FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 55342

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6822

; LENGTH: 786452

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)_(786452)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10)

US-10-719-993-6822

Query Match 21.5%; Score 34.2; DB 8; Length 786452;

Best Local Similarity 52.4%; Pred. No. 1.4e+02;

Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTCCCAATCACTCGTCTAGCTATAAGAGAGCTCAACATTGAATG 60

Db 640845 AAGGAAAAAGACTAATACATGAATTTTGAATACCTGTTAACATTTGAACAA 640786

Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATA 120

Db 129 AAGGAAAGACTAATACTGAATTCWATATTTGGAACTCTTTAAACATGAACAA 70
Qy 61 CCTCAACAGCAGCTCAAGAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAA 118
Db 69 CAACAACAAAATCCCAATATACATCTTCACTCTTCCATTTATAGAAAATTTAA 12

RESULT 26
US-10-388-838-1/c
; Sequence 1, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 170279
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(170279)
; OTHER INFORMATION: n = A, T, C or G
US-10-388-838-1

Query Match 20.5%; Score 32.6; DB 8; Length 170279;
Best Local Similarity 51.7%; Pred. No. 2.2e+02;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 15 ATACCTCAGCTCGCTCAGCTATAGAGAGGCTCAACATTTGAATGGCTCAACAGCAG 74
Db 142522 AAGCTCACATCTTTGTTATGATATAGCTCAGTTCCTTGGCACTGAATGATCACA 142463

Qy 75 TCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGAT 134
Db 142462 GAATAAGCTGCACTATATATGCACTTAAATTTGTCATGCTGTTCACACTGCCCT 142403

Qy 135 CTGTATCATCGTATGCTTCTCT 157
Db 142402 TTATTTCTTATTTGTTGACCTCT 142380

RESULT 27
US-11-029-984-845/c
; Sequence 845, Application US/11029984
; Publication No. US20050196784A1
; GENERAL INFORMATION:
; APPLICANT: Revnisdottir, Inga
; APPLICANT: Gulcher, Jeffrey R.
; APPLICANT: Grant, Struan F.
; APPLICANT: Thorleifsson, Gudmar
; TITLE OF INVENTION: Human Type II Diabetes Gene-Kv Channel-Interacting Protein (KCHIP)
; TITLE OF INVENTION: Located on Chromosome 5
; FILE REFERENCE: 2345, 2049-007
; CURRENT APPLICATION NUMBER: US/11/029,984
; CURRENT FILING DATE: 2005-01-05
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-029-984-845

Query Match 20.3%; Score 32.2; DB 10; Length 402;
Best Local Similarity 56.0%; Pred. No. 24;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 51 CATTGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTTATTTATCAATTTCTGTCT 110
Db 251 CCTAGAGTGCAGAAAAGCAAGGGTTATAAAACAGAAAATATCTATCAGTGTACCCAT 192

Qy 111 CATCTTAATATGCTCTTCTGCTGATCTGATCATCGTATGCTTCTCTCA 159
Db 191 CTCTCTGTGTCATCTCTCATCTTTGCTATATATCATCTCTCTCTTA 143

RESULT 28
US-09-925-065A-150093
; Sequence 150093, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150093
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-150093

Query Match 20.1%; Score 32; DB 4; Length 451;
Best Local Similarity 55.4%; Pred. No. 29;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 15 ATACCTCAGCTCGCTCAGCTATAGAGAGGCTCAACATTTGAATGGCTCAACAGCAG 74
Db 213 ATAGCACAGTCTCTTTCTAACAGGTCACCCACAAAAGTTGTCTCACAGCTAGAGCACT 272

Qy 75 TCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATATGCTCTC 126
Db 273 TGTAGCAAAAGAAAGTTATTTATACATTTTTTCTCATCTATAGCTTTCTC 324

RESULT 29
US-10-027-632-140279
; Sequence 140279, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

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; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140279
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-140279

Query Match      20.0%; Score 31.8; DB 5; Length 359;
Best Local Similarity 54.8%; Pred. No. 30;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 34 ATAAGAAGAGCCTCAACCAATGAAATGCCTCAACAAAGCAGCTCAAAAGCTACAGAACTCTA 93
Db 32 ATCAAAACAGCATTAACAAGTAACAGGTTTTCAAAGCTTTCTACATGCAAACTTACACA 91

QY 94 TTTATCAATTTCTGCTCATCTTAATATGCTCTCTGCTGAATCTGATCATCGTGA 148
Db 92 ATTATCCCTTTAAATTTTATCTTCTATATATATATATGATGATCTATTTGTTCTGA 146

RESULT 30
US-10-027-632-140279
; Sequence 140279, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140279
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-140279

Query Match      20.0%; Score 31.8; DB 6; Length 359;
Best Local Similarity 54.8%; Pred. No. 30;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 34 ATAAGAAGAGCCTCAACCAATGAAATGCCTCAACAAAGCAGCTCAAAAGCTACAGAACTCTA 93
Db 32 ATCAAAACAGCATTAACAAGTAACAGGTTTTCAAAGCTTTCTACATGCAAACTTACACA 91

QY 94 TTTATCAATTTCTGCTCATCTTAATATGCTCTCTGCTGAATCTGATCATCGTGA 148
Db 92 ATTATCCCTTTAAATTTTATCTTCTATATATATATGATGATCTATTTGTTCTGA 146

RESULT 31
US-09-925-065A-536994/c
; Sequence 536994, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 536994
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-536994

Query Match      20.0%; Score 31.8; DB 4; Length 636;
Best Local Similarity 59.3%; Pred. No. 38;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAAAGCAGCTCAAAAGCTACAGAACTCTATATATCAATTTCTGCTCAT 113
Db 461 TTATAAGATTTTCACATTTAAAGTGAGATGATACAGCATATGCTTTCTGCTGCTGCTTAT 402

QY 114 CTTAATATGCTCTCTGCTGATCTGTATCATC 144
Db 401 TTCACCTTAGTATAATGTTGACGCTTTCATC 371

RESULT 32
US-08-781-986A-283
; Sequence 283, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
```

```

; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-283

Query Match
Best Local Similarity 20.0%; Score 31.8; DB 2; Length 1421;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 36 AAGAGAGCCTCAACCATTTGAATTCCTCAACAGCAGCTCAAAAGCTACAGAATCTATT 95
Db 317 ACGAAGAACTGAAATTTGAAATGGGTGGATATCATGTCAAATATAGTCAAGATGTA 376
QY 96 TATCAATTCTGTCTCATCTTAA 118
Db 377 CTTCAATTACTCTATAAATAA 399

RESULT 33
US-10-329-624-283
; Sequence 283, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 283:
; US-10-329-624-283

Query Match
20.0%; Score 31.8; DB 7; Length 1421;

```

```
US-09-925-065A-719738
Query Match      19.9%; Score 31.6; DB 4; Length 812;
Best Local Similarity 62.8%; Pred. No. 48;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 65 AACAAAGCAGCTCAAAAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAATATGTC 124
Db 637 AACCAAAAGGATAAAGCTTGAGGGATGGATACCTCATCTGCTCATGATGATTTTC 578

Qy 125 TCTTGCTGATCTGTATCA 142
Db 577 ACATGTGTGCTGTATCA 560

RESULT 36
US-09-925-065A-255686/c
; Sequence 255686, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255686
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-255686

Query Match      19.7%; Score 31.4; DB 4; Length 519;
Best Local Similarity 57.7%; Pred. No. 46;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 4 GAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAAGAGCCTCAACCATTTGAATGCT 63
Db 263 GAAAAAGTCACACAACATCTTAGCACTATTATGAGAACAGCTTTGACCTTGCAACACTT 204

Qy 64 CAACAAGCAGCTCAAAAAGCTACAGAATCTATTATCA 100
Db 203 GAACATGCTCAGAAATCCTCAAGAATCTGTGAACCA 167

RESULT 37
US-09-925-065A-246839
; Sequence 246839, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246839
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-246839

Query Match      19.7%; Score 31.4; DB 4; Length 560;
Best Local Similarity 61.7%; Pred. No. 47;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 75 TCAAAAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGAT 134
Db 383 TAAAAATCTATTGATAAAATTTATCAATTTTTCCTATATACTAAAAAATCTTTTCCATAT 442

Qy 135 CTGTATCATCTGTGATGCTTCT 155
Db 443 CTATAATTAGGCATGTTTCT 463

RESULT 39
US-10-450-763-5048/c
; Sequence 5048, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11;
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 5048
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (37)..(153)
; OTHER INFORMATION: 97% homologous to Arabidopsis thaliana putative
; OTHER INFORMATION: protein, accession number AL162506, Smith-Waterman
US-10-450-763-5048 Score=193.

```

Query Match	19.7%	Score 31.4;	DB 9;	Length 873;
Best Local Similarity	53.7%	Pred. No. 57;		
Matches 65; Conservative	0;	Mismatches 56;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 40
US-10-450-763-5355/c
; Sequence 5355, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 5355
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (37)..(153)
; OTHER INFORMATION: 97% homologous to Arabidopsis thaliana putative
; OTHER INFORMATION: protein, accession number AL162506, Smith-Waterman Score=193.
US-10-450-763-5355

```

Query Match	19.7%	Score 31.4;	DB 9;	Length 873;
Best Local Similarity	53.7%	Pred. No. 57;		
Matches	65;	Conservative	0;	Mismatches 56;
				Indels 0;
				Gaps 0;

QY	37	AGAAGAGCC	TCAACCA	TGAAATG	CGCTCAAC	AAGCAGT	CAAAAGCT	CAAGAAT	CTATTT	96
Db	207	AAAAGAA	CATAACCA	TAAAAA	ATTCATAT	AGGTATT	AAAAATC	TCCCAAA	ATCATC	148
QY	97	ATCAATTC	TGCTCACT	TAAATG	TCTCTG	CTGATC	TGTCAT	CGTGCT	CTC	156
Db	147	TTCTTCT	CTCTTCT	CTCTCT	CTCCCT	CTTCTCT	CTCTCT	CTCTCT	CTCTCT	88
QY	157	T	157							
Db	87	T	87							

```

RESULT 41
US-10-450-763-11273/c
; Sequence 11273, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11273
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (361)..(948)
; OTHER INFORMATION: 87% homologous to Homo sapiens putative p150, accession number
; OTHER INFORMATION: U93563, Smith-Waterman Score=845.
US-10-450-763-11273

```

Query Match 19.7%; Score 31.4; DB 9; Length 873;
Best Local Similarity 53.7%; Pred. No. 57;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

37	AGAAGCCCTCAACCAATGCAATGCCCTCAACAGCAGCGTCAAAGGTACAGAAATCTATTT	96
Ddb		
207	AAAAGAACATAACCATTAAAAAATTCGATATAGGTATTAANAATCTTCCCAAAATCATC	148
Oy		
97	ATCAATTCTGTCTCATCTTAAATATGTCCTCTTGCTGCATCTGTATCATCGTGATGCTTCTC	156
Ddb		
147	TTCCTC	88
Oy		
157	T 157	
Ddb		
87	T 87	
Ddb		

RESULT 42
US-10-437-963-88801/c
; Sequence 88801, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88801
; LENGTH: 1199
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87617C.1
US-10-437-963-88801

Query Match 19.7%; Score 31.4; DB 7; Length 1199;
Best Local Similarity 50.3%; Pred. No. 65;
Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 3 CGAAGAAGTCCAAATACCTCAGCTCGCTCAGCTATATAAGAGAGCGCTCAAGCAATTTGAATGCC 62
DB 234 GGATGCGGTCCGGAGCTCCCTCCGGCTGATATGCTCGTCCGCTCGCGTCAATGCA 175
QY 63 TCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGTCTCATCTTAAATG 122
DB 174 TCAGCCAGCCCTTGAAGCATCCAGCTCTCTTGCGCGCGCGCGCTCATGCCGCG 115
QY 123 TCTCTGTGTGATCTGTATCATGTCATGTCATGTTCT 155
DB 114 CGTGTCTGTCTGCTTCTTCTTGTGTCGCTCT 82

RESULT 43
US-11-097-143-27115
; Sequence 27115, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27115
; LENGTH: 3505
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-27115

Query Match 19.7%; Score 31.4; DB 10; Length 3505;
Best Local Similarity 53.7%; Pred. No. 1e+02;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 22 ACTCGCTCAGCTATAAGAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAG 81

DB 2450 AGTCGCACAACTTCGACAAACCCCTTTATTTTGGAAATTAATGCTAAAAACACTTAATGAG 2509
QY 82 CTACAGAAATCTATTATCAATTTCTGTCTCACTTAATATATGCTCTTCTGCTGATCTGATC 141
DB 2510 TTGAGTTATATATTAAAGAATTTCTTTAAATATATATTAAAGATACCTTTCTGGTCAGAGTA 2569
QY 142 A 142
DB 2570 A 2570

RESULT 44
US-10-311-455-261/c
; Sequence 261, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 261
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-261

Query Match 19.7%; Score 31.4; DB 6; Length 5875;
Best Local Similarity 56.2%; Pred. No. 1.3e+02;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 21 CACTCGCTCAGCTATAAGAGAGCGCTCAACCAATTTGAAATGCTCAACAGCAGCTCAAAA 80
DB 421 CATACCTTCTCCCTTTAAAAAATACTAAATTAATATTCACCTTCAACACCACTTCAAAA 362
QY 81 GCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGCT 125
DB 361 ACTACTCACTATTATTTTCTAAATTAATTTCCCTCCCATAAATTTCT 317

RESULT 45
US-10-027-632-174763/c
; Sequence 174763, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363


```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763

```

	Query Match	19.7%	Score 31.4;	DB 5;	Length 2940917;
	Best Local Similarity	59.6%	Pred. No. 1.2e+03;		
	Matches 53;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;
Qy	59	TGCTCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCTCATCTTAA			
Db	1860510	TGCCACTAAAGGAATTTTCAGTAACTCCAAAAATTCATGCTGTATGACTGTGTGTCCTTAA			
Qy	119	TATGCTCTCTTGCTGATCTGTATCATCGTG			
Db	1860450	TATGGGCTTTTGTGCTAGATCATCTTTTG			

```

RESULT 46
US/1027-632-174763/c
; Sequence 174763, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Ma
; TITLE OF INVENTION: Polymorphisms in the
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763

```

```

; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763

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Query Match	19.7%	Score 31.4;	DB 6;	Length 2940917;
Best Local Similarity	59.6%;	Pred. No. 1.2e+03;		
Matches 53;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;
QY	59	TCGCTCAACAGCACCTCAAAACCTACAGAACTCTATTATCAATTTCTGTCATCTTAA	118	

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Db 1860510 TGCCACTAAAGGAATTTTCAGTAACTCCAAAATTCATGTCGTATGACTGTGTGTCCTTAA 1860451
QY 119 TATGTCCTCTTGGCTGATCTGTATCATCATCGTG 147
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Db 1860450 TATGGGCTTTGTCAGTCTAGATCATTTTG 1860422

RESULT 47
US-10-424-599-49155
; Sequence 49155, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 49155
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; - OTHER INFORMATION: Clone ID: PAT_MRT3847_15395C.1
US-10-424-599-49155

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Query Match	19.6%	Score 31.2;	DB 7;	Length 453;
Best Local Similarity	66.2%	Pred. No. 50;		
Matches 45;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;

QY	92	TATTTATCAATTCTCTCTCATCTTAATATGTCCTTTGGTCATCTGATCTATCATCGTGATGC	151
Db	22	TATTTAGGTATTACTCTCTCAATTTTACATGTCACCTTCTAGTTGGTCTCATTAATTAATCTC	81
QY	152	TTCTCTGA	159
Db	82	TCTTCTTA	89

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RESULT 48
US-10-087-192-712/c
; Sequence 712, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 84073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-712

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Query Match 19.6%; Score 31.2; DB 5; Length 84073;
 Best Local Similarity 58.7%; Pred. No. 4.3e+02;
 Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 37 AGAAGAGCCTCAACCAATTGAATGCTTCAACAGCAGCTCAAAGCTACAGAATCTATTT 96

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Db 28668 AGTAGAGATACAGCCACACAAAAGAAATCCAGGGTCACATAAAACCAACAGAAAGTTATCT 28609
QY 97 ATCAATTTCTGTCATCTTATATGTCCTT 128
Db 28608 AACCAACCTTTGAATCTTGTAAATCTGAGTCTT 28577

RESULT 49
US-10-027-632-233567/c
; Sequence 233567, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233567
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-233567

Query Match 19.5%; Score 31; DB 5; Length 633;
Best Local Similarity 72.7%; Pred. No. 66;
Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 89 ATCTATTATCAATTTCTGTCATCTTATATGTCCTTCTGTCATCTGATCTGATCAT 143
Db 178 ATATAATTATATATTGTTATCATCATATATATCTATCTACTACTCATCTGTATGAT 124

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Job time : 819 secs
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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233567
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-233567

Query Match 19.5%; Score 31; DB 6; Length 633;
Best Local Similarity 72.7%; Pred. No. 66;
Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 89 ATCTATTATCAATTTCTGTCATCTTAAATATGTCCTTCTGTCATCTGATCTGATCAT 143
Db 178 ATATAATTATATATTGTTATCATCATATATCTATCTACTACTCATCTGTATGAT 124

Search completed: December 8, 2005, 04:24:50
Job time : 819 secs
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 02:14:01 ; Search time 648 Seconds

(without alignments)
91.733 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atggagaaagtccaatacct.....tcacgtgatctctctga 159

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	20.0	150038	7	US-11-121-086-23
2	31.4	19.7	1844	6	US-10-750-185-64456
3	31	19.5	1256	6	US-10-750-185-48936
4	30.2	19.0	958	6	US-10-750-185-44270
5	29	18.2	172147	7	US-11-112-908-22
6	29	18.2	188682	7	US-11-112-908-32
7	28.8	18.1	193363	7	US-11-112-908-32
8	28.4	17.9	2618	6	US-10-750-185-42442
9	28.2	17.7	1005	6	US-10-750-185-42220
10	28.2	17.7	1025	6	US-10-750-185-32974
11	27.8	17.5	600	6	US-10-750-185-917
12	27.8	17.5	1327	6	US-10-750-185-60655
13	27.6	17.4	748	6	US-10-750-185-52599
14	27.6	17.4	744	6	US-10-750-185-54343
15	27.6	17.4	1301	6	US-10-750-185-26340
16	27.6	17.4	1749	6	US-10-750-185-62610
17	27.6	17.4	3105	6	US-10-750-185-51145
18	27.4	17.2	1183	6	US-10-750-185-51145
19	27.4	17.2	1305	6	US-10-750-185-51810
20	27.4	17.2	2317	6	US-10-750-185-51810
21	27.4	17.2	2563	6	US-10-750-185-37324
22	27.4	17.2	156544	7	US-11-121-086-81
23	27.4	17.2	170837	7	US-11-121-086-97

17.2	171423	7	US-11-121-086-85	Sequence 85, Appl
17.1	666	6	US-10-793-626-2777	Sequence 2777, Ap
17.1	864	6	US-10-750-185-52881	Sequence 52881, A
17.1	4136	6	US-10-793-626-3686	Sequence 3686, Ap
17.1	196200	7	US-11-121-086-9	Sequence 9, Appli
17.1	246960	7	US-11-121-086-8	Sequence 8, Appli
17.1	319608	7	US-11-145-703-1	Sequence 1, Appli
17.0	742	6	US-10-793-626-2981	Sequence 2981, Ap
17.0	2116	6	US-10-750-185-36690	Sequence 36690, A
17.0	2332	6	US-10-750-185-57047	Sequence 57047, A
17.0	2744	6	US-10-750-185-30659	Sequence 30659, A
17.0	3048	6	US-10-793-626-3660	Sequence 3660, Ap
17.0	3163	6	US-10-793-626-3889	Sequence 3889, Ap
17.0	4113	6	US-10-624-932-21	Sequence 21, Appli
17.0	5855	7	US-11-108-528-27	Sequence 27, Appli
17.0	212805	7	US-11-112-908-19	Sequence 19, Appli
16.9	1229	6	US-10-750-185-26323	Sequence 26323, A
16.9	1320	6	US-10-750-185-55086	Sequence 55086, A
16.9	1733	6	US-10-750-185-33223	Sequence 33223, A
16.9	3617	6	US-10-131-826A-409	Sequence 409, App
16.9	3627	6	US-10-750-185-35364	Sequence 35364, A
16.9	138821	7	US-11-121-086-80	Sequence 80, Appli
16.9	139054	7	US-11-121-086-96	Sequence 96, Appli
16.9	156735	7	US-11-121-086-93	Sequence 93, Appli
16.7	847	6	US-10-750-185-32215	Sequence 32215, A
16.7	1197	7	US-11-112-908-135	Sequence 135, App
16.7	1256	6	US-10-750-185-30040	Sequence 30040, A
16.7	1524	6	US-10-750-185-47853	Sequence 47853, A
16.7	1573	6	US-10-750-185-55695	Sequence 55695, A
16.7	2057	6	US-10-750-185-60135	Sequence 60135, A
16.7	2079	6	US-10-750-185-52763	Sequence 52763, A
16.7	2915	6	US-10-750-185-49578	Sequence 49578, A
16.7	3040	6	US-10-793-626-3789	Sequence 3789, Ap
16.7	3204	6	US-10-793-626-4294	Sequence 4294, Ap
16.7	3994	6	US-10-793-626-3496	Sequence 3496, Ap
16.7	4605	6	US-10-750-185-32760	Sequence 32760, A
16.7	180862	7	US-11-112-908-40	Sequence 40, Appli
16.7	190882	7	US-11-121-086-50	Sequence 50, Appli
16.7	203467	7	US-11-121-086-69	Sequence 69, Appli
16.6	1672	6	US-11-121-086-50	Sequence 50, Appli
16.6	2016	6	US-10-750-185-60433	Sequence 60433, A
16.6	159497	7	US-11-112-908-61	Sequence 61, Appli
16.6	162173	7	US-11-121-086-72	Sequence 72, Appli
16.6	185393	7	US-11-121-086-69	Sequence 101, App
16.5	600	6	US-10-750-185-2944	Sequence 2944, Ap
16.5	1008	6	US-10-750-185-62885	Sequence 62885, A
16.5	1546	6	US-10-750-185-32954	Sequence 32954, A
16.5	1557	6	US-10-750-185-53487	Sequence 53487, A
16.5	1751	6	US-10-750-185-45716	Sequence 45716, A
16.5	2271	6	US-10-750-185-41450	Sequence 41450, A
16.5	3331	6	US-11-000-463-8	Sequence 8, Appli
16.5	3690	7	US-11-000-463-8	Sequence 8, Appli
16.5	85682	7	US-11-117-187-205	Sequence 205, App
16.5	163317	7	US-11-117-187-212	Sequence 212, App
16.5	165627	7	US-11-121-086-89	Sequence 89, Appli
16.5	176503	7	US-11-121-086-53	Sequence 53, Appli
16.5	611587	7	US-11-117-187-209	Sequence 209, App
16.4	1253	6	US-10-750-185-35340	Sequence 35340, A
16.4	1461	6	US-10-750-185-53487	Sequence 53487, A
16.4	1577	6	US-10-750-185-45716	Sequence 45716, A
16.4	1613	6	US-10-750-185-41450	Sequence 41450, A
16.4	2105	7	US-11-054-385-11	Sequence 11, Appli
16.4	3198	6	US-10-750-185-63042	Sequence 63042, A
16.4	3730	6	US-10-485-517-116	Sequence 116, App
16.4	150468	7	US-11-112-908-56	Sequence 56, Appli
16.4	151828	7	US-11-117-187-197	Sequence 197, App
16.4	172781	7	US-11-112-908-25	Sequence 25, Appli
16.4	177175	7	US-11-121-086-79	Sequence 79, Appli
16.4	179777	7	US-11-121-086-106	Sequence 106, App
16.4	193789	7	US-11-112-908-55	Sequence 55, Appli
16.4	235033	7	US-11-157-389-1	Sequence 1, Appli
16.4	237326	7	US-11-157-389-2	Sequence 2, Appli
16.4	260209	6	US-10-933-025-23	Sequence 23, Appli

c 97 25.8 16.2 600 6 US-10-750-185-3836 Sequence 3836, Ap
c 98 25.8 16.2 600 6 US-10-750-185-20094 Sequence 20094, A
c 99 25.8 16.2 600 6 US-10-750-185-21310 Sequence 21310, A
c 100 25.8 16.2 743 6 US-10-750-185-31770 Sequence 31770, A

ALIGNMENTS

RESULT 1

US-11-121-086-23
; Sequence 23, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23
; LENGTH: 150038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-23

Query Match 20.0%; Score 31.8; DB 7; Length 150038;
Best Local Similarity 54.8%; Pred. No. 8.2; Indels 0; Gaps 0;
Matches 63; Conservative 0; Mismatches 52;
QY 34 ATAAGAGAGCCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTA 93
DB 10677 ATCAAAACAGCATTAAACAGTAAACAGGTTTCAAGGCTTCTACATGCACACTTACACA 10736
QY 94 TTATCAATTTCTGCTCATCTTTAATATGCTCTTCTGCTGATCGTATCATCGTGA 148
DB 10737 ATATCCCTTAAATTTTATCTTCATATATATGATGATGATCTATTTGTTCTGA 10791

RESULT 2

US-10-750-185-64456/c
; Sequence 64456, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 64456
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Bovine 19866880659967
US-10-750-185-64456

Query Match 19.7%; Score 31.4; DB 6; Length 1844;
Best Local Similarity 59.6%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 36;

QY 38 GAAGAGCCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTTA 97
DB 128 GACAGGACTGAGCGACTGAACAATAACAAAGTAATCAAGAACCAACTGTCTCTATTTA 69
QY 98 TCATTTCTGCTCATCTTAAATATGCTC 126
DB 68 TGAATTAATTTCTTAACCTTCGTATTCAC 40

RESULT 3

US-10-750-185-48936/c
; Sequence 48936, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48936
; LENGTH: 1256
; TYPE: DNA
; ORGANISM: Bovine 19866880996475
US-10-750-185-48936

Query Match 19.5%; Score 31; DB 6; Length 1256;
Best Local Similarity 72.7%; Pred. No. 2.8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 15;
QY 104 TCTGCTCATCTTAATATGCTCTTCTGCTCATCTGTATCATCGTATCGTCTCTG 158
DB 68 TCTGCCACAGACTAATATGTAATCTTCTTCTTCATCATAGTATGATGATGCTG 14

RESULT 4

US-10-750-185-44270
; Sequence 44270, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 44270
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Bovine 19866881864870
US-10-750-185-44270

Query Match 19.0%; Score 30.2; DB 6; Length 958;
Best Local Similarity 58.2%; Pred. No. 4.4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 38;

QY 51 CATTGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTTATTTCAATTTCTGTCT 110
Db 834 CATTGATATTTCTCATTGAACAACTTTTACAACTTGTAGGATTTATAGTGTGATGTGTGT 893
QY 111 CATCTTAATATGCTCTTCTGCTGATCTGATC 141
Db 894 AAATGAAGAAGTCCCGAAGTCTTTTACC 924

RESULT 5
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

Query Match 18.2%; Score 29; DB 7; Length 172147;
Best Local Similarity 53.0%; Pred. No. 58;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 10 GTCCATACCTCACTCGCTCAGCTATTAAGAGAGCCTCAACAACTGAAATGCTCAACAA 69
Db 140767 GTGAACGTACCTGCTCAAACTGGTGTAGCAAAATCAACAAATTTGTTGCAACAACAG 140826
QY 70 GCACGTCAAAAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAATATGCTCTC 126
Db 140827 CAACAACACACAAAGAAATCTTTTTTTTTTTTGTAGTCTGTCTGTCTAC 140883

RESULT 6
US-11-112-908-23
; Sequence 23, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 188682

; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-23
Query Match 18.2%; Score 29; DB 7; Length 188682;
Best Local Similarity 53.0%; Pred. No. 59;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 10 GTCCATACCTCACTCGCTCAGCTATTAAGAGAGCCTCAACAACTGAAATGCTCAACAA 69
Db 90388 GTGAACGTACCTGCTCAAACTGGTGTAGCAAAATCAACAAATTTGTTGCAACAACAG 90447
QY 70 GCACGTCAAAAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAATATGCTCTC 126
Db 90448 CAACAACACACAAAGAAATCTTTTTTTTTTTTGTAGTCTGTCTGTCTAC 90504

RESULT 7
US-11-112-908-32/c
; Sequence 32, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 193363
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-32

Query Match 18.1%; Score 28.8; DB 7; Length 193363;
Best Local Similarity 65.6%; Pred. No. 69;
Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 77 AAAAGCTACAGAACTTATTTATCAATTTCTGCTCATCTTAATATGCTCTGCTGATCT 136
Db 13416 AATAGTCACAGAGTGGTTATCATTGCTTTCTTCTTCTTTCTTTCTTCTTCTTCT 13357
QY 137 GTAT 140
Db 13356 TTCT 13353

RESULT 8
US-10-750-185-42442
; Sequence 42442, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

```
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42442
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Bovine 19866881135702
US-10-750-185-42442

Query Match      17.9%; Score 28.4; DB 6; Length 2618;
Best Local Similarity 54.9%; Pred. No. 21;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 58 ATGCTCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTA 117
Db 2082 ATTCATAAGCAATATTTTCAAAAAATACACAGTACTATTAAACCTATTTTATCACT 2141

QY 118 ATATGCTCTCTGCTGATCTGATCATCGTGATGCTTCTCTGA 159
Db 2142 TAATGCTTAATGCTTATCGCTTTTGTATTATAAATACGACATGA 2183

RESULT 9
US-10-750-185-42320
; Sequence 42320, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42320
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Bovine 19866880600062
US-10-750-185-42320

Query Match      17.7%; Score 28.2; DB 6; Length 1005;
Best Local Similarity 53.1%; Pred. No. 17;
Matches 60; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 39 AAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTAT 98
Db 277 AAGAGATGAAGAGAGAGAGAGCTCAAGACAACTTCAAGTTTCGAGCTGTGATGT 336

QY 99 CAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTATCATCTGTATGC 151
Db 337 AATGGCTCGTCCATGCTGATTTTATTGTTTACTTTTATCATCTGTAATGC 389

RESULT 10
US-10-750-185-32974/c
; Sequence 32974, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
```

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; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32974
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Bovine 19866881951924
US-10-750-185-32974

Query Match      17.7%; Score 28.2; DB 6; Length 1025;
Best Local Similarity 57.3%; Pred. No. 18;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 CAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGT 123
Db 488 CAGCAGCAACCTAATATTATAAAAAATCTATTTCCTCAATCTACTTAGACAGTTATTCAG 429

QY 124 CTCCTTGCTGATCTGATCATCTGATGCT 152
Db 428 TTCCTTACAGATCTGTTTCATCATATTGAT 400

RESULT 11
US-10-750-185-917
; Sequence 917, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 917
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT02074
US-10-750-185-917

Query Match      17.5%; Score 27.8; DB 6; Length 600;
Best Local Similarity 51.2%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 31 GCTATAGAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCTCAAAAGCTACAGAA 90
Db 250 GGTTTAAAAAGAAATGTTGATATTATTTGTTTAAATGAGAGAAACAAWATAAGAG 309

QY 91 CTATTTATCAATTTCTGCTCATCTTAAATATGCTCTTGTGCTGATCTGTATCATCTGATG 150
Db 310 CTACCCCTCCCTTTTCAGTTTTTTTCTTTTACTCTTACAAATCTTTGTTACTGTTGAA 369

QY 151 CTCTCTCT 157
Db 370 GTTCTTT 376

RESULT 12
US-10-750-185-60655
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; Sequence 60655, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60655
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Bovine 19866881277196
US-10-750-185-60655

Query Match      17.5%; Score 27.8; DB 6; Length 1327;
Best Local Similarity 51.2%; Pred. No. 25;
Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 31 GCTATAAGAGAGCTCAACCATTAATGCTCTCAACAGCAGCTCAAAAGCTACAGAA 90
DB 622 GGTATAAAGAGAGTGTATTAATGTAATGGTTTAAATGAGAGAAACAAATAAGAG 681

QY 91 CTATTTATCAATTTCTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATG 150
DB 682 CTACCTCCCTTTTCAGTTTTTTTCTTCTTACTCTTCAAACTTTGTTACTGTGAA 741

QY 151 CTCTCT 157
DB 742 GTCTCT 748

RESULT 13
US-10-750-185-52599
; Sequence 52599, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 52599
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Bovine 19866882169195
US-10-750-185-52599

Query Match      17.4%; Score 27.6; DB 6; Length 738;
Best Local Similarity 58.5%; Pred. No. 24;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 73 COTCAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGTTCTTGTG 132
DB 731 CTTCTCT 132

; Sequence 60655, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60655
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Bovine 19866881277196
US-10-750-185-60655

Query Match      17.5%; Score 27.8; DB 6; Length 1327;
Best Local Similarity 51.2%; Pred. No. 25;
Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 31 GCTATAAGAGAGCTCAACCATTAATGCTCTCAACAGCAGCTCAAAAGCTACAGAA 90
DB 622 GGTATAAAGAGAGTGTATTAATGTAATGGTTTAAATGAGAGAAACAAATAAGAG 681

QY 91 CTATTTATCAATTTCTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATG 150
DB 682 CTACCTCCCTTTTCAGTTTTTTTCTTCTTACTCTTCAAACTTTGTTACTGTGAA 741

QY 151 CTCTCT 157
DB 742 GTCTCT 748

RESULT 14
US-10-750-185-54343/c
; Sequence 54343, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54343
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Bovine 19866880609777
US-10-750-185-54343

Query Match      17.4%; Score 27.6; DB 6; Length 744;
Best Local Similarity 53.8%; Pred. No. 24;
Matches 57; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 52 ATTGAATGCTCAACAGCAGCTCAAAAGCTCAAGAACTATTATCAATTTCTGCTC 111
DB 736 AGTGAATTTCTGAGAGCGCTGCACCACCAAGGACAAAGATTTATTGCAAGTTTGCCTT 677

QY 112 ATCTTAATATGCTCTTCTGATCTGTATCATCTGTATCATCGTGCTCTCT 157
DB 676 TTCTTCTTTTCTTATTCACACTTGTAAAATTGGACTGTGACTGT 631

RESULT 15
US-10-750-185-26340
; Sequence 26340, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26340
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Bovine 19866880707421
US-10-750-185-26340

Query Match      17.4%; Score 27.6; DB 6; Length 1301;
```

Best Local Similarity 53.8%; Pred. No. 29;
Matches 57; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAGCTACAGAACTCT 92
Db 1177 TAGAATATGCAACTTAAATGATTGAATGATCAACAAGACATGGCTAGCTACAGATGAA 1236
QY 93 ATTATCAATTCTCTCATCTCAATTAATATGCTCTTGTCTGATCTGT 138
Db 1237 TGTTCATATGACTATATGTCATCTCAGATGATCTGCTTATTTAT 1282

RESULT 16
US-10-793-626-1079
; Sequence 1079, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1079

Query Match 17.4%; Score 27.6; DB 6; Length 1749;
Best Local Similarity 60.8%; Pred. No. 32;
Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAGCTACAGAACTCT 92
Db 468 TGTCAAAGAAGATATTACCAATTAATGCTTAAAGAGTACCACCAATATATCTCAAGT 527
QY 93 ATTATCAATTCTCT 106
Db 528 ATTTAAAGATATTT 541

RESULT 17
US-10-793-626-4436/c
; Sequence 4436, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4436
; LENGTH: 3105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4436
Query Match 17.4%; Score 27.6; DB 6; Length 3105;
Best Local Similarity 60.8%; Pred. No. 39;

Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAGCTACAGAACTCT 92
Db 669 TGTCAAAGAAGATATTACCAATTAATGCTTAAAGAGTACCACCAATATATCTCAAGT 610
QY 93 ATTATCAATTCTCT 106
Db 609 ATTTAAAGATATTT 596

RESULT 18
US-10-750-185-51145/c
; Sequence 51145, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51145
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Bovine 19866880950653
US-10-750-185-51145

Query Match 17.2%; Score 27.4; DB 6; Length 1183;
Best Local Similarity 52.1%; Pred. No. 32;
Matches 61; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 43 GCCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAAT 102
Db 883 GCCTGTACCATGACTATGACATAACTTACTTTAAAAATGAAATGTTAGTATGTATAAG 824
QY 103 TTCTGTCTCATCTTAATATGCTCTTGTGCTGATCTGTATCATCTGTATGCTTCTCTGA 159
Db 823 TCCTTTGAGGAGTAAATAAATCCCTTATAATGACAGCTATTGAGGCTTCTCTGA 767

RESULT 19
US-10-750-185-51810/c
; Sequence 51810, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51810
; LENGTH: 1305
; TYPE: DNA


```
; ORGANISM: Bovine 19866880706323
US-10-750-185-51810

Query Match      17.2%; Score 27.4; DB 6; Length 1305;
Best Local Similarity 50.4%; Pred. No. 33;
Matches 67; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGTCCAAATACCTCAGCTGCTAGCTATAGAAAGAGCCTCAACCATGGAAGTCCCTCAACA 68
Db 1093 AATTAATAATCATCACCCTCAGGATAGAGTAGTCTTCAACTCTGACAATCACTGACA 1034

QY 69 AGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATATGTCCTTT 128
Db 1033 GAAATATTAAAGGTCAGAAATGATGATACATATATTTCTGTTTATTATGATTAT 974

QY 129 GCTGATCTGTATC 141
Db 973 AAAGATGTGACTC 961

RESULT 20
US-10-750-185-59493/c
; Sequence 59493, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59493
; LENGTH: 2317
; TYPE: DNA
; ORGANISM: Bovine 19866880953651
US-10-750-185-59493

Query Match      17.2%; Score 27.4; DB 6; Length 2317;
Best Local Similarity 65.6%; Pred. No. 40;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 96 TATCAATTTCTGCTCATCTTAATATGCTCTCTGCTGATCTGATCATGCTGATGCTTCT 155
Db 1027 TATCTTTTCTGTTTATACATATTTCTTATGTTTCATGAGCATCATATATGTTGATTC 968

QY 156 C 156
Db 967 C 967

RESULT 21
US-10-750-185-37324
; Sequence 37324, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2

; ORGANISM: Bovine 19866880819128
US-10-750-185-37324

Query Match      17.2%; Score 27.4; DB 6; Length 2563;
Best Local Similarity 69.8%; Pred. No. 42;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 107 GTCTCATCTTAATATGCTCTTCTGCTGATCTCTATCATGCTGATGCTTCTCTGA 159
Db 2307 GTCACCTCTTGAAGTGAAGTCTTCTGCTGATCTCTTAATATGATCAAGCTGCGTTTA 2359

RESULT 22
US-11-121-086-81
; Sequence 81, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KRISTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-81

Query Match      17.2%; Score 27.4; DB 7; Length 156544;
Best Local Similarity 59.7%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 48 AACCATTTGAAATGCCCTCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTG 107
Db 1093 AACCTTAGAAGTAAATTCAGTAAAGTTGCCAAATACAGATCAACCTATAAAATCAG 1152

QY 108 TCTCATCTTAATATGTC 124
Db 1153 TAGCATTCTATATGTC 1169

RESULT 23
US-11-121-086-97/c
; Sequence 97, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KRISTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 170837
; TYPE: DNA
```

US-11-121-086-97

ORGANISM: Homo sapiens

Query Match 17.2%; Score 27.4; DB 7; Length 170837;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 55; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 44 CCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATT 103
DB 19319 COTCCACGATTGTGAGGCTCCCGCCAGCATGTGTAAGTCCAAATAAACCTCTT 19260

QY 104 TCTGTCTCATCTTAATATGTCTCTTGGCTGATCTGTATCATC 144
DB 19259 TCTTTGTAATGCCAGTCTCAGGTATGCTTTATCAGC 19219

RESULT 24

US-11-121-086-85

Sequence 85, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 85
LENGTH: 171423
TYPE: DNA
ORGANISM: Homo sapiens

US-11-121-086-85

Query Match 17.2%; Score 27.4; DB 7; Length 171423;
Best Local Similarity 53.2%; Pred. No. 1.7e+02;
Matches 58; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 15 ATACCTCAGTCGCTCAGCTATAGAAGAGCTCAACATTAAGTGAATGCTCAACAGCAGC 74
DB 40019 AAAACACGTTTCAAAAAAATAAATCTGTAGGACTGATAAACAATCTCTATAAG 40078

QY 75 TCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATGT 123
DB 40079 TTGTAGTTTACAAAATCAACATATCAATATCAGTAGCATTCTATATAT 40127

RESULT 25

US-10-793-626-2777/c

Sequence 2777, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2777
LENGTH: 666
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence

US-10-793-626-2777

US-10-750-185-52881

Sequence 52881, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52881
LENGTH: 864
TYPE: DNA
ORGANISM: Bovine 19866881283242

US-10-750-185-52881

Query Match 17.1%; Score 27.2; DB 6; Length 864;
Best Local Similarity 50.8%; Pred. No. 33;
Matches 65; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCCCTCAACCATTTGAAATG 60
DB 373 ATACAAAAAAGCTTCTCTTTAGTAGGACCAACCAAAACCAATAAATGATACAAATGAAAT 432

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
DB 433 TAAAAAATAAATAAAGCAACCTTCTTAAACAATGAACAAACCTGTATTTTCGTATT 492

QY 121 TGTCTCTT 128
DB 493 TTTCTGTT 500

RESULT 27

US-10-793-626-3686

Sequence 3686, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3686
LENGTH: 4136
TYPE: DNA

us-10-691-412-1-1.rnpbn

Query Match 17.1%; Score 27.2; DB 6; Length 4136;
Best Local Similarity 64.1%; Pred. No. 56;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 94 TTTATCAATTTCTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTATGCTT 153
DB 3518 TTTCTCAAGTCATCTTTTTCATAATACGCCTTAGATGATCTATAGCATATTGTGCATC 3577

QY 154 CTCT 157
DB 3578 TTCT 3581

RESULT 28
US-11-121-086-9/c
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-9

Query Match 17.1%; Score 27.2; DB 7; Length 196200;
Best Local Similarity 51.7%; Pred. No. 2e+02;
Matches 62; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 9 AGTCCATACCTCACTCGCTCAGCTATATAAGAGAGCTCAACATTTGAATGGCTCAACA 68
DB 163955 ATTGAAACCTGAATCTTGAGCTTTTCAGTTTGCAAAACTCTTCACCTACCCACCA 163896

QY 69 AGCACGTCAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATATGCTCTT 128
DB 163895 CACATATCAACATTTTGTATATATATATATATATATATATATATATATATATAT 163836

RESULT 29
US-11-121-086-8/c
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

us-10-691-412-1-1.rnpbn

Query Match 17.1%; Score 27.2; DB 7; Length 246960;
Best Local Similarity 51.7%; Pred. No. 2.1e+02;
Matches 62; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 9 AGTCCATACCTCACTCGCTCAGCTATATAAGAGAGCTCAACATTTGAATGGCTCAACA 68
DB 39091 ATTGAAACCTGAATCTTGAGCTTTTCAGTTTGCAAAACTCTTCACCTACCCACCA 39032

QY 69 AGCACGTCAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATATGCTCTT 128
DB 39031 CACATATCAACATTTTGTATATATATATATATATATATATATATATATATATATAT 38972

RESULT 30
US-11-145-703-1/c
; Sequence 1, Application US/11145703
; Publication No. US2005026067A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Esicoux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:

LOCATION: 230408..230721	OTHER INFORMATION: exon P complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 231272..231412	OTHER INFORMATION: exon Obis complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 231787..231880	OTHER INFORMATION: exon O2 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 231870..231879	OTHER INFORMATION: exon O1 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 234174..234321	OTHER INFORMATION: exon O complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 237406..237428	OTHER INFORMATION: exon Nb1s complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 239719..239807	OTHER INFORMATION: exon N2 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 239719..239853	OTHER INFORMATION: exon N complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240569	OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240596	OTHER INFORMATION: exon M1090 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240617	OTHER INFORMATION: exon M1069 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240644	OTHER INFORMATION: exon MS2 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240824	OTHER INFORMATION: exon M862 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240994	OTHER INFORMATION: exon M692 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..241685	OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:	
NAME/KEY: exon	
LOCATION: 240800..240993	OTHER INFORMATION: exon MS1 complement g34872 gene
FEATURE:	
NAME/KEY: misc feature	
LOCATION: 241686..243685	OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:	
NAME/KEY: misc feature	
LOCATION: 290652..292652	OTHER INFORMATION: 3'regulatory region g34665 gene
Query Match	17.1%; Score 27.2; DB 7; Le
Best Local Similarity	55.2%; Pred. No. 2.2e+02;

Query Match 17.1%; Score 27.2; DB 7; Length 319608;
Best Local Similarity 55.2%; Pred. No. 2.2e+02;

Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 23 CTCGCTAGCTATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGC 82
Db 73738 CTAAATCAGTTGTAAGAGGAACTTTTCATCTTTTAATGCTATATTAGAAATAGCAAA 73679
QY 83 TACAGATCTATTATCAATTTCTGTCATCTTAA 118
Db 73678 GTCTAAATCAGTTATCATCTATGCTTTTATCTTAA 73643
RESULT 31
US-10-793-626-2981
; Sequence 2981, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2981
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2981

Query Match 17.0%; Score 27; DB 6; Length 742;
Best Local Similarity 55.0%; Pred. No. 36;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 30 AGCTATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGCTACAGRA 89
Db 556 AGATAAAGGAATGAGTAAGATTAGATTTCATATTAGTACATCAGCGCTAAAAAA 615
QY 90 TCATTATCAATTTCTGTCATCTTAA 120
Db 616 GTTCAACAACAATTTCTGTTATTCGGAATA 646

RESULT 32
US-10-750-185-36690
; Sequence 36690, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36690
; LENGTH: 2116
; TYPE: DNA
; ORGANISM: Bovine 1986680917915
US-10-750-185-36690

Query Match 17.0%; Score 27; DB 6; Length 2116;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 5 AGAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATGCTC 64
Db 707 AAAAAATCCAATTCGCCCAATTCAGCTATAATTTGAACAGCCCAACAGACAGCCAA 766
QY 65 AACAGAGCAGCTCAA 79
Db 767 AACCAATCATGAAAAA 781

RESULT 33
US-10-750-185-57047/c
; Sequence 57047, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57047
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Bovine 1986680788543
US-10-750-185-57047

Query Match 17.0%; Score 27; DB 6; Length 2332;
Best Local Similarity 51.2%; Pred. No. 53;
Matches 63; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGCTACAGAACT 92
Db 1575 TGTAAATGAAACCAACCAATCAAGGGGCTTAAGGATCATCGCTGATCTCCCTTAGCA 1516
QY 93 ATTATCAATTTCTGTCATCTTATATATGCTCTTGTGATCTGTATCATCTGATGCT 152
Db 1515 ACTAGTTTCTAGCTGTGCTAGCTTAGAATTACTATTAAATGTTGAATTAATTATGAT 1456
QY 153 TCT 155
Db 1455 TTT 1453

RESULT 34
US-10-750-185-30659/c
; Sequence 30659, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482


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; LENGTH: 4113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-21

Query Match
Best Local Similarity 17.0%; Score 27; DB 6; Length 4113;
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 20 TCATCGCTCAGCTATAAGAGAGCGCTCAACCAATGAAATGCTCAACAGCAGCAGTCAAA 79
Db 3934 TAACAATCTAGCTTTTAAAGAGAACTATTATGTAATAATTTCTACATGTCATTCAGA 3993
QY 80 AGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTA 139
Db 3994 TATTATGATATCTTCTAGCGCTTTATCTGTACTTTTAAATGATACATATTTCTGCTGCG 4053
QY 140 TCATCGCTGATGCTTCTCTG 158
Db 4054 TGATTTGATATTTCACTG 4072

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RESULT 36
US-11-108-528-27
; Sequence 27, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE OF INVENTION: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2005-04-16
; PRIOR FILING DATE: 2004-04-16
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5855
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-108-528-27

```

```

Query Match
Best Local Similarity 17.0%; Score 27; DB 7; Length 5855;
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 20 TCATCGCTCAGCTATAAGAGAGCGCTCAACCAATGAAATGCTCAACAGCAGCAGTCAAA 79
Db 3759 TAACAATCTAGCTTTTAAAGAGAACTATTATGTAATAATTTCTACATGTCATTCAGA 3818
QY 80 AGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTA 139
Db 3819 TATTATGATATCTTCTAGCGCTTTATCTGTACTTTTAAATGATACATATTTCTGCTGCG 3878
QY 140 TCATCGCTGATGCTTCTCTG 158
Db 3879 TGATTTGATATTTCACTG 3897

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RESULT 39
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US2005026059A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole

```

```

; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

```

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Query Match
Best Local Similarity 17.0%; Score 27; DB 7; Length 212805;
Matches 66; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATGAAATGCTCAACAGCAGCAGTCAAAAGCTACA 86
Db 198354 CTCAGCTTCCAAAGTCTCGAATTACAGGCGTGAGCCAGCCGCGCTAGCTTATT 198413
QY 87 GAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGATCATCGT 146
Db 198414 ATTTACCTTTTCATTTCTTCTATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 198473
QY 147 GATGCTTCTCT 157
Db 198474 TTTAATTTCTGT 198484

```

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RESULT 40
US-10-750-185-26323/c
; Sequence 26323, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26323
; LENGTH: 1229
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-26323

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Query Match
Best Local Similarity 16.9%; Score 26.8; DB 6; Length 1229;
Matches 52; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 29 CAGCTATAAGAGAGCGCTCAACCAATGAAATGCTCAACAGCAGCAGTCAAAAGCTACA 88
Db 174 CAGGCATCACTAGAGTCTCAGTGGGAAGGTGAAGATCAGCAAGATACAGTGTACGC 115
QY 89 ATCTATTTATCAATTTCTGCTCATCTTAATATG 122

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Db	114	AACCTTGGAATATGCTGTTTAATGTTCAATG	81
RESULT 41			
US-10-750-185-55086			
; Sequence 55086, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIN version 3.1			
; SEQ ID NO 55086			
; LENGTH: 1320			
; TYPE: DNA			
; ORGANISM: Bovine 19866880846515			
US-10-750-185-55086			
Query Match 16.9%; Score 26.8; DB 6; Length 1320;			
Best Local Similarity 57.0%; Pred. No. 50;			
Matches 49; Conservative 0; Mismatches 37; Indels 0; Gaps 0;			
Qy	74	GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCACTTAATATCTCTCTGCTGA	133
Db	699	GTAACATGCTATACATGATGTACAAATGTAATATCTCTTATATCATTTATTTGTTCT	758
Qy	134	TCTGTATCATCGTGATGCTTCTCTGA	159
Db	759	TATGAGAATTTATGTGCGCATGACTTA	784
RESULT 42			
US-10-750-185-33223			
; Sequence 33223, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIN version 3.1			
; SEQ ID NO 33223			
; LENGTH: 1733			
; TYPE: DNA			
; ORGANISM: Bovine 19866880464123			
US-10-750-185-33223			
Query Match 16.9%; Score 26.8; DB 6; Length 1733;			
Best Local Similarity 49.3%; Pred. No. 55;			
Matches 70; Conservative 0; Mismatches 72; Indels 0; Gaps 0;			
Qy	12	CCATACCTCACTCGCTCAGCTATAAGAAGAGCCTCAACCATTCGAAATGCCTCAACAAGC	71
Db	1054	CAATACCTCATACTTACATATATGAGGTGTTCCAGGAAAAATGAAAAACAAGAATAAT	1113
Qy	72	ACGTCAAAAAGCTACAGAAATCTATTATTAATTTCTGCTCATCTTAATATATGCTCTTGCT	131
Db	1114	AAACCAAAACAAAAAAGAAAAAACAACAACTGTTCCAGCAGACAGAAAGATGGGTTCCG	1173
Qy	132	GATCTGTATCATCGTGATGCTT	153
Db	1174	GAATTTCTAATTCAGTTGGTT	1195
RESULT 43			
US-10-131-826A-409/c			
; Sequence 409, Application US/10131826A			
; Publication No. US20050245730A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3330RIC128			
; CURRENT APPLICATION NUMBER: US/10/131,826A			
; CURRENT FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: 60/049911			
; PRIOR FILING DATE: 1997-06-18			
; PRIOR APPLICATION NUMBER: 60/056974			
; PRIOR FILING DATE: 1997-08-26			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059115			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059117			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059122			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059184			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059263			
; PRIOR FILING DATE: 1997-09-18			
; PRIOR APPLICATION NUMBER: 60/059352			
; PRIOR FILING DATE: 1997-09-19			
; PRIOR APPLICATION NUMBER: 60/059588			
; PRIOR FILING DATE: 1997-09-19			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 409			
; LENGTH: 3617			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-131-826A-409			
Query Match 16.9%; Score 26.8; DB 6; Length 3617;			
Best Local Similarity 55.3%; Pred. No. 71;			
Matches 52; Conservative 0; Mismatches 42; Indels 0; Gaps 0;			
Qy	63	TCAAAGCAGCGTCAAAAGTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATG	122

Db 1685 TCAGCAATCATGTTTAAATTAACATAACATGATTATTAACTGTTGACAGATATTAACTTG 1626

QY 123 TCTCTTCTGATCTGTATCATCTCGTGATGCTTCTC 156

Db 1625 ACAGATCACTATTAAAAATAAACTTATTTTACCTC 1592

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RESULT 44
US-10-750-185-35364/c
; Sequence 35364, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35364
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-35364

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	Query Match	16.9%	Score 26.8	DB 6	Length 3627
	Best Local Similarity	52.7%	Pred. No. 71		
	Matches	58	Conservative 0	Mismatches 52	Indels 0
	Gaps	0			
QY	19	CTCACTCGCTCAGCTATAGAAAGCGCTCAACCAATTGAAATGGCTCAACAGCACGTCAA	78		
Db	3534	CACAGACACATATATGTATAGAAAAATTAATCTTAAACCCACAAATAGAAACATCAG	3475		
QY	79	AAGCTACAGAANTCTATTTATCAATTTCTGCTCATCTTAATATGTCCTT	128		
Db	3474	AAAGGTAGACGTGTTTATGTTATTTCTGCAACCTCTGAATAGCTTCCTT	3425		

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RESULT 45
US-11-121-086-80
; Sequence 80, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80
; LENGTH: 138821
; TYPE: DNA
; ORGANISM: Homo sapiens
JS-11-121-086-80

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Query Match 16.9%; Score 26.8; DB 7; Length 138821;
Best Local Similarity 55.3%; Pred. No. 2.3e+02;
Matches 52; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
30 AGCTATAAGAGACCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAA 89

Accession	Sequence	Position
Db	62237 AACTATAAGGGATCTGAGACCAACAGTTTGAGACTGATGGTTTACGGCTACAAAT	62396
Qy	90 TCTATTATCAATTTCTGTCCTCATCTTTAATATGT	123
Db	62297 TCAATTATCACAAATATGACTTTGAATATATTT	62330

RESULT 46

```

US-11-121-086-96/c
; Sequence 96, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/557,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 139054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-96

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	Query Match	Best Local Similarity	16.9%;	Score 26.8;	DB 7;	Length 139054;
	Matches	Conservative	55.3%;	Pred. No. 2.3e+02;	Mismatches 42;	Indels 0; Gaps 0;
QY	44	CCTCAACCATTTGAATGGCTCTCAACAGCACGCTCAAAAGCTACAGAACTCTATTTATCAATT	103			
Db	52932	CGTGAACCTCTCTAGATGAAGCAACAATTTGAGTAAATCTTACAGAATCCAATCATCTAGG				
QY	104	TCTGTCTCATCTTAAATATGTCTCTTGGCTGATCTG	137			
Db	52872	GCTGACCCCTACATATAATTGAAATTTGGCTATGTG	52839			

RESULT 47

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US-11-121-086-93
; Sequence 93, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 156735
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-93

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	Query Match	16.9%;	Score 26.8;	DB 7;	Length 156735;
	Best Local Similarity	52.7%;	Pred. No. 2.4e+02;		
	Matches 58;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;
31	GCTATAAGAGAGCGCTCAACCATTTGAATGCTTCAACGAGCAGCTCAAAAGCTACAGAAAT	90			
75555	GCCAAAAGACAAATCATTCAGACACCCGCTATGCGACGAGAAATGGAAAGCAGGAGAAAT	77614			
91	CTATTATCAATTTCTGTCTCATCTTAATATGCTCTTGTGTACTGTAT	140			

Db	77615	AAATTTATATTTCTGTCAAATTGTTACATGAAATTTATTTTATATAT	77664
RESULT 48			
US-10-750-185-32215/c			
; Sequence 32215, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 32215			
; LENGTH: 847			
; TYPE: DNA			
; ORGANISM: Bovine 19866881406535			
US-10-750-185-32215			
Query Match 16.7%; Score 26.6; DB 6; Length 847;			
Best Local Similarity 63.1%; Pred. No. 49;			
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
Qy	28	TCAGCTATAGAGAGCGCTCAACATTGAATGCCCTCAACAGCAGCTCAAAAGCTACAG	87
Db	211	TCAGATATATACGCTGCTAAATCAATGAGTGACTCTATCAACATTTATCAAGATACAG	152
Qy	88	AATCT 92	
Db	151	AAGCT 147	
RESULT 49			
US-11-112-908-135/c			
; Sequence 135, Application US/11112908			
; Publication No. US20050260659A1			
; GENERAL INFORMATION:			
; APPLICANT: Harris, Cole			
; APPLICANT: Davis, Lisa M.			
; TITLE OF INVENTION: Breast Cancer Biomarkers			
; FILE REFERENCE: 04-164-US			
; CURRENT APPLICATION NUMBER: US/11/112,908			
; CURRENT FILING DATE: 2005-04-22			
; PRIOR APPLICATION NUMBER: US 60/564,758			
; PRIOR FILING DATE: 2004-04-23			
; PRIOR APPLICATION NUMBER: US 60/575,978			
; PRIOR FILING DATE: 2004-06-01			
; PRIOR APPLICATION NUMBER: US 60/631,702			
; PRIOR FILING DATE: 2004-11-30			
; PRIOR APPLICATION NUMBER: US 60/633,826			
; PRIOR FILING DATE: 2004-12-07			
; NUMBER OF SEQ ID NOS: 511			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 135			
; LENGTH: 1197			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-112-908-135			
Query Match 16.7%; Score 26.6; DB 7; Length 1197;			
Best Local Similarity 58.0%; Pred. No. 55;			
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
Qy	77	AAAAGCTACAGAACTCTATTTATCAATTTCTGCTCACTTAATATATCTCTTGTCTGATCT	136
Db	583	AAAAGTTACATGATTGATGGGAAATTTTATTTCTCATCATATTAAGATATTTTAATCAT	524
Qy	137	GTATCATCGTGATGCTTCTCT	157
Db	523	TTGTTAAACCTGGAGATATTTCT	503
RESULT 50			
US-10-750-185-30040			
; Sequence 30040, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 30040			
; LENGTH: 1256			
; TYPE: DNA			
; ORGANISM: Bovine 19866881910681			
US-10-750-185-30040			
Query Match 16.7%; Score 26.6; DB 6; Length 1256;			
Best Local Similarity 48.4%; Pred. No. 56;			
Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Qy	5	AGAAAGTCCAATACCTCACTCGCTCAAGCTATAGAAGAGCGCTCAACCAATTGAAATGCCCTC	64
Db	278	AGAAGGGACAAGTCATAGGTTTATTTTAATAGGAGATCTCTAATGACTTGTTCCTT	337
Qy	65	AACAAGCAGCTCAAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTTAATATGTC	124
Db	338	CACAGTTAACTTTTAAGAAACCATGTTATTTTATTTATATTTGTTATATTTTGCACACTGT	397
Qy	125	TCTTGTCTGATCTGTATCATCGTGATGCTTCTCT	157
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Job time : 654 Secs			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 23:56:51 ; Search time 3746 Seconds
(without alignments)
1985.891 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atgagaaagtccaataacct.....tcacgtgatgcttctctga 159

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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: gb_est2.*
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8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	100.0	159	11	DQ046231
2	159	100.0	376	5	C05636
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4	159	100.0	408	1	AL600669
5	159	100.0	412	1	AL601169
6	159	100.0	412	5	C04012
7	159	100.0	426	1	AJ710051
8	159	100.0	426	7	CN411469
9	159	100.0	431	1	AL601173
10	159	100.0	433	1	AL600088
11	159	100.0	438	5	C02888
12	159	100.0	443	1	AI190578
13	159	100.0	448	5	C03252
14	159	100.0	451	5	C04050
15	159	100.0	455	1	AL601166
16	159	100.0	477	1	AL599208
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33	159	100.0	551	3	BP259965
34	159	100.0	552	1	AL600429
35	159	100.0	552	3	BP259458
36	159	100.0	553	3	BP257543
37	159	100.0	554	3	BP258625
38	159	100.0	556	3	BP257310
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42	159	100.0	559	3	BP260265
43	159	100.0	560	3	BP257291
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45	159	100.0	561	3	BP257982
46	159	100.0	561	3	BP258939
47	159	100.0	562	3	BP257744
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51	159	100.0	563	3	BP259242
52	159	100.0	563	3	BP259967
53	159	100.0	564	3	BP257798
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58	159	100.0	565	3	BP258858
59	159	100.0	565	3	BP260005
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67	159	100.0	568	3	BP258837
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73	159	100.0	570	3	BP259093
74	159	100.0	571	3	BP257806
75	159	100.0	571	3	BP258451
76	159	100.0	571	3	BP258954
77	159	100.0	572	3	BP257207
78	159	100.0	572	3	BP260018
79	159	100.0	573	3	BP258250
80	159	100.0	573	3	BP260038
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95	159	100.0	580	3	BP257104

96	159	100.0	580	3	BP257141	BP257141
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RESULT 1	DQ046231	159 bp	DNA	linear	GSS 02-JUN-2005	
LOCUS	DQ046231	159 bp	DNA	linear	GSS 02-JUN-2005	
DEFINITION	Homo sapiens PLN gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.					
ACCESSION	DQ046231	1	GI:66897446			
VERSION	DQ046231	1	GI:66897446			
KEYWORDS	GSS.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 159) Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Cividello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees					
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)					
PUBMED	15869325					
AUTHORS	2 (bases 1 to 159) Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Cividello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.					
FEATURES	source					
gene	1..159 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" <1..>159 /gene="PLN" /locus_tag="HC12009"					
ORIGIN	Location/Qualifiers					
Query Match	100.0%;	Score 159;	DB 11;	Length 159;		
Best Local Similarity	100.0%;	Pred. No. 7.2e-35;				
Matches 159;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	ATGAGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGAGCCTCAACCAATTGAAATG 60				
Db	1	ATGAGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGAGCCTCAACCAATTGAAATG 60				
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120				
Db	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120				
QY	121	TGTCCTTTGCTGATCTGTATCATCGTATGCTTCTCTGA 159				
Db	121	TGTCCTTTGCTGATCTGTATCATCGTATGCTTCTCTGA 159				
RESULT 2	C05636	376 bp	mRNA	linear	EST 30-JUL-1996	
LOCUS	C05636	376 bp	mRNA	linear	EST 30-JUL-1996	
DEFINITION	Human heart cDNA (YNakamura) Homo sapiens cDNA clone					

3NHC5059,	mRNA sequence.
C05636	
C05636.1	GI:1468887
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 376) Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE	Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
JOURNAL	Genomics 35 (1), 231-235 (1996)
PUBMED	8661126
COMMENT	Contact: Yusuke Nakamura Institute of Medical Science University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan Tel: 81-3-5449-5372 Fax: 81-3-5449-5433 Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES	Location/Qualifiers
source	1..376 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="3NHC5059" /dev_stage="adult" /clone_lib="Human heart cDNA (YNakamura)" /note="Organ: heart; normalized directionally cloned cDNA from adult heart"
ORIGIN	Query Match 100.0%; Score 159; DB 5; Length 376; Best Local Similarity 100.0%; Pred. No. 8.2e-35; Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGCCTCAACCAATTGAAATG 60
Db	182 ATGGAGAAAGTCCAAATACCTCAGTCTAGCTATAGAGAGCCTCAACCAATTGAAATG 241
QY	61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
Db	242 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
QY	121 TGTCCTTTGCTGATCTGTATCATCGTATGCTTCTCTGA 159
Db	302 TGTCCTTTGCTGATCTGTATCATCGTATGCTTCTCTGA 340
RESULT 3	AL599452
LOCUS	AL599452
DEFINITION	383 bp mRNA linear EST 04-SEP-2003 DKFZp313N0529 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION	AL599452
VERSION	AL599452.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 383) Bloeker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.
TITLE	EST (Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.

This clone (DKFp313N0529) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..383
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFp313N0529"
/dev_stage="adult"
/lab_host="DH10B"
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/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 383;
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Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 60
|||||
Db 143 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 202
|||||
QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
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Db 203 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 262
|||||
QY 121 TGTCTCTTGTGATCTGTATCATCGTGAGCTTCTCTGA 159
|||||
Db 263 TGTCTCTTGTGATCTGTATCATCGTGAGCTTCTCTGA 301
|||||

RESULT 4

AL600669
LOCUS DKFp31302134 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION DKFp31302134 5', mRNA sequence.

ACCESSION AL600669
VERSION AL600669.1 GI:15164175
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

AUTHORS 1 (bases 1 to 408)
Ansoorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.

TITLE EST (Ansoorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES

Location/Qualifiers
1..408
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFp31302134"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

This clone (DKFp31302134) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..408

/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 408;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 60
|||||

Db 142 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 201
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QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
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Db 202 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 261
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGAGCTTCTCTGA 159
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Db 262 TGTCTCTTGTGATCTGTATCATCGTGAGCTTCTCTGA 300
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RESULT 5

AL601169
LOCUS DKFp313C1140 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION DKFp313C1140 5', mRNA sequence.

ACCESSION AL601169
VERSION AL601169.1 GI:15164675
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

AUTHORS 1 (bases 1 to 412)
Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and

Wiemann, S.

TITLE EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and

Wiemann, S.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

This clone (DKFp313C1140) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..412
/organism="Homo sapiens"
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cDNA-collection"

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Best Local Similarity	100.0%;	Pred. No. 8.3e-35;			
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				Gaps	0;
QY	1	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	60		
Db	126	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	185		
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	120		
Db	186	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	245		
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159		
Db	246	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	284		
RESULT 6					
LOCUS	C04012	Human heart cDNA (YNakamura)	Homo sapiens	cDNA clone	
DEFINITION	3NHC2551,	mRNA sequence.			
ACCESSION	C04012				
VERSION	C04012.1	GI:1467263			
KEYWORDS	EST.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
	1 (bases 1 to 412)				
	Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and				
	Nakamura,Y.				
TITLE	Construction of a normalized directionally cloned cDNA library from				
	adult heart and analysis of 3040 clones by partial sequencing				
JOURNAL	Genomics 35 (1), 231-235 (1996)				
PUBMED	8661126				
COMMENT	Contact: Yusuke Nakamura				
	Institute of Medical Science				
	University of Tokyo				
	4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan				
	Tel: 81-3-5449-5372				
	Fax: 81-3-5449-5433				
	Email: yusuke@ims.u-tokyo.ac.jp.				
FEATURES					
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	/clone_lib="Human heart cDNA (YNakamura)"				
	/note="Organ: heart; normalized directionally cloned cDNA				
	from adult heart"				
ORIGIN					
Query Match	100.0%;	Score 159;	DB 5;	Length 412;	
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				Indels	0;
				Gaps	0;
QY	1	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	60		
Db	184	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	243		
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	120		
Db	244	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	303		
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159		
Db	304	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	342		

Query Match	100.0%;	Score 159;	DB 1;	Length 412;	
Best Local Similarity	100.0%;	Pred. No. 8.3e-35;			
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				Gaps	0;
QY	1	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	60		
Db	126	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	185		
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	120		
Db	186	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	245		
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159		
Db	246	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	284		
RESULT 6					
LOCUS	C04012	Human heart cDNA (YNakamura)	Homo sapiens	cDNA clone	
DEFINITION	3NHC2551,	mRNA sequence.			
ACCESSION	C04012				
VERSION	C04012.1	GI:1467263			
KEYWORDS	EST.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
	1 (bases 1 to 412)				
	Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and				
	Nakamura,Y.				
TITLE	Construction of a normalized directionally cloned cDNA library from				
	adult heart and analysis of 3040 clones by partial sequencing				
JOURNAL	Genomics 35 (1), 231-235 (1996)				
PUBMED	8661126				
COMMENT	Contact: Yusuke Nakamura				
	Institute of Medical Science				
	University of Tokyo				
	4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan				
	Tel: 81-3-5449-5372				
	Fax: 81-3-5449-5433				
	Email: yusuke@ims.u-tokyo.ac.jp.				
FEATURES					
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	/note="Organ: heart; normalized directionally cloned cDNA				
	from adult heart"				
ORIGIN					
Query Match	100.0%;	Score 159;	DB 5;	Length 412;	
Best Local Similarity	100.0%;	Pred. No. 8.3e-35;			
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				Indels	0;
				Gaps	0;
QY	1	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	60		
Db	184	ATGGAGAAAGTCCAAATCACTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAATG	243		
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	120		
Db	244	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	303		
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159		
Db	304	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	342		

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 426 Std Error: 0.00.
 Location/Qualifiers
 1. 426
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 /note="Foligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic acid and mitogens."

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 Best Local Similarity 100.0%; Pred. No. 8.3e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 107 ATGAGAGAAAGTCCAAATACCTCAGCTATAGAGAGAGCTCAACCATTTGAATG 166
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 DB 167 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTCTCATCTTAATA 226
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RESULT 9
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 VERSION
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 SOURCE
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 431)
 Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.
 EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.)
 Unpublished (1999)
 Contact: MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No si sequence available.
 This clone (DKFZp313C0340) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1. 431
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FEATURES
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ORIGIN
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 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTCTCATCTTAATA 120
 DB 203 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTCTCATCTTAATA 262
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
 DB 263 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 301

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 433)
 Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.
 EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.)
 Unpublished (1999)
 Contact: MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No si sequence available.
 This clone (DKFZp313C1332) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1. 433
 /organism="Homo sapiens"
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 cDNA-collection"

FEATURES
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 Query Match 100.0%; Score 159; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 8.3e-35;
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 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTCTCATCTTAATA 120
 DB 203 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTCTCATCTTAATA 262
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QY	1	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG	60
Db	141	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG	200
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QY	121	TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA	159
Db	261	TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA	299
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LOCUS	C02888	438 bp mRNA linear	EST 30-JUL-1996
DEFINITION	C02888 Human heart cDNA (YNakamura)	Homo sapiens cDNA clone	
ACCESSION	3NHCO465	mRNA sequence.	
VERSION	C02888		
KEYWORDS	C02888.1	GI:1466139	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1	(bases 1 to 438)	
AUTHORS	Tanaka,T., Ogiwara,A., Uchiyama,I., Takegi,T., Yazaki,Y. and Nakamura,Y.		
TITLE	Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing		
JOURNAL	Genomics 35 (1), 231-235 (1996)		
PUBMED	8661126		
COMMENT	Contact: Yusuke Nakamura Institute of Medical Science University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan Tel: 81-3-5449-5372 Fax: 81-3-5449-5433 Email: yusuke@ims.u-tokyo.ac.jp.		
FEATURES	Location/Qualifiers		
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ORIGIN			
Query Match	100.0%;	Score 159;	DB 5; Length 438;
Best Local Similarity	100.0%;	Pred. No. 8.4e-35;	
Matches	159;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG	60
Db	182	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG	241
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATTAATTAATTTCTCATCTTAATA	120
Db	242	CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATTAATTAATTTCTCATCTTAATA	301
QY	121	TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA	159
Db	302	TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA	340
RESULT 12			
LOCUS	A1190578/c	443 bp mRNA linear	EST 28-OCT-1998
DEFINITION	q66e07.x1 Soares_testis_NHT	Homo sapiens cDNA clone IMAGE:1733892	

3' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN); mRNA sequence.

ACCESSION A1190578

VERSION A1190578.1

GI:3741787

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 443)

AUTHORS NCI-CGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 654 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers

source 1..443

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1733892"

/sex="male"

/lab_host="DH10B"

/clone_lib="Soares testis NHT"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 443;

Best Local Similarity 100.0%; Pred. No. 8.4e-35;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG 60

Db 421 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATTAAGAAGAGCCTCAACCAATTGAAATG 362

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 120

Db 361 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 302

QY 121 TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA 159

Db 301 TGTCCTTTGCTGATCTGTATCATCTGTATCGTCTCTCTGA 263

RESULT 13

LOCUS C03252

448 bp mRNA linear EST 30-JUL-1996

DEFINITION C03252 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHCI144, mRNA sequence.

ACCESSION C03252

VERSION C03252.1

GI:1466503

KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
PUBMED 8661126
COMMENT Contact: Yusuke Nakamura
 Institute of Medical Science
 University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
 Tel: 81-3-5449-5372
 Fax: 81-3-5449-5433
 Email: yusuke@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1. 448
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="3NHCI144"
 /dev_stage="adult"
 /note="Organ: heart; normalized directionally cloned cDNA from adult heart"

FEATURES
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 1. 448
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="3NHCI144"
 /dev_stage="adult"
 /note="Organ: heart; normalized directionally cloned cDNA from adult heart"

ORIGIN
 Query Match 100.0%; Score 159; DB 5; Length 448;
 Best Local Similarity 100.0%; Pred. No. 8.4e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 60
 DB 184 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 243
 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 244 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 303
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 159
 DB 304 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 342

RESULT 14
C04050
LOCUS C04050 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone
DEFINITION 3NHCI2620, mRNA sequence.
ACCESSION C04050
VERSION C04050.1 GI:1467301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
PUBMED 8661126
COMMENT Contact: Yusuke Nakamura
 Institute of Medical Science
 University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
 Tel: 81-3-5449-5372

FEATURES
 source
 1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="3NHCI2620"
 /dev_stage="adult"
 /note="Organ: heart; normalized directionally cloned cDNA from adult heart"

ORIGIN
 Query Match 100.0%; Score 159; DB 5; Length 451;
 Best Local Similarity 100.0%; Pred. No. 8.4e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 60
 DB 161 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 220
 QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 221 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 280
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 159
 DB 281 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 319

RESULT 15
AL601166
LOCUS AL601166
DEFINITION DKFP313B0340 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION AL601166
VERSION AL601166.1 GI:15164672
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No sl sequence available.
 This clone (DKFP313B0340) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1. 455
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFP313B0340"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /note="Vector: piriplex2; Site_1: SfiIA; Site_2: SfiIB;

ORIGIN		cDNA-collection"	
Query Match		100.0%; Score 159; DB 1; Length 455;	
Best Local Similarity		100.0%; Pred. No. 8.4e-35;	
Matches 159; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	60
DB	142	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	201
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	120
DB	202	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	261
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159
DB	262	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	300
RESULT 16			
AL599208			
LOCUS		477 bp mRNA linear EST 04-SEP-2003	
DEFINITION		DKFZp313D2225_r1_313 (synonym: hlcc2) Homo sapiens cDNA clone	
ACCESSION		DKFZp313D2225 5', mRNA sequence.	
VERSION		AL599208	
KEYWORDS		EST.	
SOURCE		AL599208.1 GI:15162496	
ORGANISM		Homo sapiens (human)	
REFERENCE		1 (bases 1 to 477)	
AUTHORS		Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).	
TITLE		EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: MIPS	
FEATURES		Location/Qualifiers	
source		1..477	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="DKFZp313D2225"	
		/dev_stage="adult"	
		/lab_host="DH10B"	
		/clone_lib="313 (synonym: hlcc2)"	
		/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"	
		100.0%; Score 159; DB 1; Length 477;	
		Best Local Similarity 100.0%; Pred. No. 8.5e-35;	
		Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	60
DB	201	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	260
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	120
ORIGIN			
Query Match		100.0%; Score 159; DB 1; Length 478;	
Best Local Similarity		100.0%; Pred. No. 8.5e-35;	
Matches 159; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	60
DB	142	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	201
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	120
DB	202	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	261
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159
DB	262	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	300
RESULT 17			
AL600135			
LOCUS		478 bp mRNA linear EST 04-SEP-2003	
DEFINITION		DKFZp313F1932_r1_313 (synonym: hlcc2) Homo sapiens cDNA clone	
ACCESSION		DKFZp313F1932 5', mRNA sequence.	
VERSION		AL600135	
KEYWORDS		EST.	
SOURCE		AL600135.1 GI:15163446	
ORGANISM		Homo sapiens (human)	
REFERENCE		1 (bases 1 to 478)	
AUTHORS		Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.).	
TITLE		EST (Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.).	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: MIPS	
FEATURES		Location/Qualifiers	
source		1..478	
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		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="DKFZp313F1932"	
		/dev_stage="adult"	
		/lab_host="DH10B"	
		/clone_lib="313 (synonym: hlcc2)"	
		/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"	
		100.0%; Score 159; DB 1; Length 478;	
		Best Local Similarity 100.0%; Pred. No. 8.5e-35;	
		Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	60
DB	142	ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCAATTGAAATG	201
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	120
DB	202	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA	261
QY	121	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	159
DB	262	TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA	300
RESULT 18			
AL601279			
LOCUS		479 bp mRNA linear EST 04-SEP-2003	

DEFINITION DKFZp331L1640_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
 ACCESSION DKFZp331L1640 5', mRNA sequence.
 VERSION AL601279
 KEYWORDS EST, mRNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE This is the 5' sequence of the clone insert
 JOURNAL Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 COMMENT sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 81 sequence available.
 This clone (DKFZp331L1640) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..479
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp331L1640"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /notes="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 8.5e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
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 Db 196 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
 |||||

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120
 |||||
 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 19
 AL601190
 LOCUS DKFZp331D0840_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
 DEFINITION DKFZp331D0840 5', mRNA sequence.
 ACCESSION AL601190
 VERSION AL601190.1 GI:15164696
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE This is the 5' sequence of the clone insert
 JOURNAL Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 COMMENT sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 81 sequence available.
 This clone (DKFZp331L1640) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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 1..482
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp331D0840"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /notes="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
 Query Match 100.0%; Score 159; DB 1; Length 482;
 Best Local Similarity 100.0%; Pred. No. 8.5e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
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 Db 196 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
 |||||

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120
 |||||
 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 20
 AJ708798
 LOCUS AJ708798 CPMF001 Homo sapiens cDNA clone CPMF03862, mRNA sequence.
 DEFINITION AJ708798
 ACCESSION AJ708798
 VERSION AJ708798.1 GI:49503093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE This is the 5' sequence of the clone insert
 JOURNAL Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 COMMENT sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 81 sequence available.
 This clone (DKFZp331D0840) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..533
 /organism="Homo sapiens"
 /mol_type="mRNA"

AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 81 sequence available.
 This clone (DKFZp331D0840) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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 1..482
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp331D0840"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /notes="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
 Query Match 100.0%; Score 159; DB 1; Length 482;
 Best Local Similarity 100.0%; Pred. No. 8.5e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
 |||||
 Db 196 ATGGAGAAAGTCCAAATACCTCCTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
 |||||

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120
 |||||
 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 20
 AJ708798
 LOCUS AJ708798 CPMF001 Homo sapiens cDNA clone CPMF03862, mRNA sequence.
 DEFINITION AJ708798
 ACCESSION AJ708798
 VERSION AJ708798.1 GI:49503093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.
 TITLE Expression profiling of human hypertrophic cardiomyopathy progressed to dilated cardiomyopathy by DNA microarray analysis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Millino C
 Biology and CRIBI
 University of Padova
 Via U. Bassi, 58/B, 35131, ITALY.
 Location/Qualifiers
 1..533
 /organism="Homo sapiens"
 /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="CMPD03862"
/tissue_type="heart"
/clone_lib="CMPD01"
/note="caucasian"

ORIGIN
Query Match 100.0%; Score 159; DB 1; Length 533;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAAATG 60
|||||
Db 168 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAAATG 227
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Qy 61 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||
Db 228 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 287
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Qy 121 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
|||||
Db 288 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 326
|||||

RESULT 21
LOCUS C03682 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone
DEFINITION 3NHC2016, mRNA sequence.
ACCESSION C03682
VERSION C03682.1 GI:1466933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 533)
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library from
adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
PUBMED 8661126
COMMENT Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES
Location/Qualifiers
1..533
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="3NHC2016"
/dev_stage="adult"
/clone_lib="Human heart cDNA (Ynakamura)"
/note="Organ: heart; normalized directionally cloned cDNA
from adult heart"

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Query Match 100.0%; Score 159; DB 5; Length 533;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAAATG 60
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Db 185 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAAATG 244
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Qy 61 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
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/db_xref="taxon:9606"
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/clone_lib="CMPD01"
/note="caucasian"

Db 245 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 304
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Qy 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
|||||
Db 305 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 343
|||||

RESULT 22
AJ709272
LOCUS AJ709272 CMPD01 Homo sapiens cDNA clone CMPD04718, mRNA sequence.
DEFINITION AJ709272
ACCESSION AJ709272
VERSION AJ709272.1 GI:49503567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 534)
AUTHORS Millino,C.
TITLE Expression profiling of human hypertrophic cardiomyopathy
progressed to dilated cardiomyopathy by DNA microarray analysis
JOURNAL Unpublished (2004)
COMMENT Contact: Millino C
Biotechnology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.
FEATURES
Location/Qualifiers
1..534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CMPD04718"
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/clone_lib="CMPD01"
/note="caucasian"

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Query Match 100.0%; Score 159; DB 1; Length 534;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 180 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGTATAAGAGAGCCTCAACCAATTGAAATG 239
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Qy 61 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||
Db 240 CCTCAACAGCAGGTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 299
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Qy 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
|||||
Db 300 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 338
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RESULT 23
AL600427
LOCUS AL600427 540 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFP313J1533_r1.313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFP313J1533 5', mRNA sequence.
ACCESSION AL600427
VERSION AL600427.1 GI:15163933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 540)
AUTHORS Koehler,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
```

COMMENT

Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No s1 sequence available.
This clone (DKFZp313J1533) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313J1533"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 60
DB 183 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 242
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 120
DB 243 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 302
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTATCGTCTCTGA 159
DB 303 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 341

RESULT 24

AJ712160
LOCUS AJ712160 CIMP01 Homo sapiens cDNA clone CIMP10425, mRNA sequence.
DEFINITION AJ712160 541 bp mRNA linear EST 30-JUN-2004
ACCESSION AJ712160
VERSION AJ712160.1 GI:49506455
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 541)
Millino,C.
Expression profiling of human hypertrophic cardiomyopathy
progressed to dilated cardiomyopathy by DNA microarray analysis
Unpublished (2004)
Contact: Millino C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1..541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CIMP10425"
/tissue_type="heart"
/clone_lib="CIMP01"
/note="Caucasian"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 541;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
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QY 1 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 60
DB 194 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 253
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 120
DB 254 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 313
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
DB 314 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 352

RESULT 25

AL600196
LOCUS AL600196
DEFINITION DKFZp313J2432_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION AL600196
VERSION AL600196.1 GI:15163702
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 543)
Bloecher,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
Wiemann,S.
EST (Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
Wiemann,S.)
Unpublished (1999)
Contact: MIPS

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

Location/Qualifiers

1..543

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp313J2432"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="313 (synonym: hlcc2)"

/note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313J2432) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Query Match 100.0%; Score 159; DB 1; Length 543;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 60
DB 164 ATGGAGAAGTCCAAATACCTCAGCTCGCTAGTATAAGAGAGCCTCAACATTGAATG 223
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 120

Db 224 CCTCAAGCAGCTCAAGAGCTACAGAACTATTTATCAATTTCTGTCATCTTAATA 283
QY 121 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 159
Db 284 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 322

RESULT 26
AL600489 547 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP31302033 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION DKFP31302033 5', mRNA sequence.
ACCESSION AL600489
VERSION AL600489.1 GI:15163995
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BNFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No 5' sequence available.
This clone (DKFP31302033) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source Location/Qualifiers
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/clone_lib="313 (synonym: hlcc2)"
/notes="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATA 120
Db 267 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATA 326
QY 121 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 159
Db 327 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 365

RESULT 27
AJ708988 548 bp mRNA linear EST 30-JUN-2004
LOCUS AJ708988
DEFINITION AJ708988 CMPD01 Homo sapiens cDNA clone CMPD04183, mRNA sequence.
ACCESSION AJ708988

VERSION AJ708988.1 GI:49503283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 548)
AUTHORS Millino,C.
TITLE Expression profiling of human hypertrophic cardiomyopathy
progressed to dilated cardiomyopathy by DNA microarray analysis
JOURNAL Unpublished (2004)
COMMENT Contact: Millino C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.
FEATURES source Location/Qualifiers
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QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATA 120
Db 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCATCTTAATA 314
QY 121 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 159
Db 315 TGTCTCTGCTGATCTGATCATCTGATGCTGATGCTTCTCTGA 353

RESULT 28
BP257178 550 bp mRNA linear EST 16-SEP-2004
LOCUS BP257178 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION HRT00312, mRNA sequence.
ACCESSION BP257178
VERSION BP257178.1 GI:52172408
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT 1532556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasuuki@ims.u-tokyo.ac.jp.
FEATURES source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
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QY 121 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
DB 314 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 352

RESULT 29
BP259966
LOCUS
DEFINITION
BP259966 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT08389, mRNA sequence.
ACCESSION
BP259966
VERSION
BP259966.1 GI:52175196
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

FEATURES
source
1..550
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Sugano cDNA library, heart"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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DB 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGTCTCATCTTAATA 314
QY 121 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
DB 315 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 353

RESULT 31
BP260274
LOCUS
DEFINITION
BP260274 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT09384, mRNA sequence.
ACCESSION
BP260274
VERSION
BP260274.1 GI:52175505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

FEATURES
source
1..550
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Sugano cDNA library, heart"

ORIGIN
Query Match      100.0%; Score 159; DB 3; Length 550;
Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGGCTCAACCAATTGAATG 60
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DB 227 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGTCTCATCTTAATA 286
QY 121 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
DB 287 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 325

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RESULT 30
BP260039
LOCUS
DEFINITION
BP260039 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT08583, mRNA sequence.
ACCESSION
BP260039
VERSION
BP260039.1 GI:52175269
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..550
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT08583"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN
Query Match      100.0%; Score 159; DB 3; Length 550;
Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGGCTCAACCAATTGAATG 60
DB 195 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATATAAGAGGCTCAACCAATTGAATG 254
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGTCTCATCTTAATA 120
DB 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGTCTCATCTTAATA 314
QY 121 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 159
DB 315 TGTCTCTTCTGATCTGTATCATCGTATCATCGTATCTCTCTGA 353

RESULT 31
BP260274
LOCUS
DEFINITION
BP260274 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT09384, mRNA sequence.
ACCESSION
BP260274
VERSION
BP260274.1 GI:52175505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

```

```
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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Db 283 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 321
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DEFINITION
HRT05807, mRNA sequence.
ACCESSION
BP259171
VERSION
BP259171.1 GI:52174401
KEYWORDS
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SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 551)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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RESULT 34
AL600429 Homo sapiens
LOCUS
DEFINITION
DKFZ313J1933_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION
AL600429
VERSION
AL600429.1 GI:15163935
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.
TITLE EST (Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMPZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZ313J1933) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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DB 293 TGTCTCTTGTGATCTGATCATCGTATCGTATCGTCTCTCTGA 331

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DEFINITION BP259458 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT06808, mRNA sequence.
ACCESSION BP259458
VERSION BP259458.1 GI:52174688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
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QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
DB 195 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 254

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

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DB 241 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 300
QY 121 TGTCTCTTGTGATCTGATCATCGTATCGTATCGTCTCTCTGA 159
DB 301 TGTCTCTTGTGATCTGATCATCGTATCGTATCGTCTCTCTGA 339

RESULT 36

BP257543
LOCUS BP257543 553 bp mRNA linear EST 16-SEP-2004
DEFINITION BP257543 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT01211, mRNA sequence.
ACCESSION BP257543
VERSION BP257543.1 GI:52172773
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 553)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

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DB 195 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 254

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QY 121 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353
RESULT 37
LOCUS BP258625 Sugano cDNA library, heart Homo sapiens cDNA clone EST 16-SEP-2004
DEFINITION HRT04008, mRNA sequence.
ACCESSION BP258625
VERSION BP258625.1 GI:52173855
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353
RESULT 38
LOCUS BP257310 Sugano cDNA library, heart Homo sapiens cDNA clone EST 16-SEP-2004
DEFINITION HRT00632, mRNA sequence.
ACCESSION BP257310
VERSION BP257310.1 GI:52172540
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Db 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATCTTAATA 314
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Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353
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DEFINITION HRT03359, mRNA sequence.
ACCESSION BP258394
VERSION BP258394.1 GI:52173624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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 DB 315 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 353
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RESULT 40
 BP258989

LOCUS BP258989 558 bp mRNA linear EST 16-SEP-2004
 DEFINITION BP258989 Sugano cDNA library, heart Homo sapiens cDNA clone
 HRT05216, mRNA sequence.

ACCESSION BP258989
 VERSION BP258989
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 558)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PubMed 15342556

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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RESULT 41
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 DEFINITION as84a05.x1 Barstead colon HPLR7 Homo sapiens cDNA clone
 IMAGE:2335376 3', similar to gb:M63603 CARDIAC PHOSPHOLAMBAN
 (HUMAN);, mRNA sequence.

ACCESSION AI720214.1 GI:5037470
 VERSION AI720214
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 559)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

TITLE WashU-NCI human EST Project
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

FEATURES
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 TGTTAGCATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 [5'-AATCACTAGTAAT 3' and 5'-ATTACTAGT 3'], digested
 with Not I and cloned into the Not I and Eco RI sites of
 the modified pT7T3 vector. Library constructed by Bob
 Barstead."

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 559;
 Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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 DB 298 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 260
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RESULT 42
 BP260265

LOCUS BP260265 559 bp mRNA linear EST 16-SEP-2004
 DEFINITION BP260265 Sugano cDNA library, heart Homo sapiens cDNA clone
 HRT09360, mRNA sequence.

ACCESSION BP260265

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VERSION      BP260265.1  GI:52175496
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1 (bases 1 to 559)
AUTHORS     Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE       Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL      Genome Res. 14 (9), 1711-1718 (2004)
PUBMED      15342556
COMMENT     Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.

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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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QY      61  CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 120
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DB      264 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 323
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QY      121 TGTCTCTTGTGATCTGTATCATCTGTCATCTGTCCTGA 159
         |||||||
DB      324 TGTCTCTTGTGATCTGTATCATCTGTCATCTGTCCTGA 362
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RESULT 44
AL600477      561 bp mRNA linear EST 04-SEP-2003
LOCUS         DKFp313N2433_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION    DKFp313N2433 5', mRNA sequence.
ACCESSION     AL600477
VERSION       AL600477.1 GI:15163983
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE     1 (bases 1 to 561)
AUTHORS       Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
TITLE         EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL       Unpublished (1999)
COMMENT       Contact: MIPS
             MIPS
             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
             This is the 5' sequence of the clone insert
             Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
             Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
             sequenced by BMFZ (Biomedical Research Center at the Charite,
             Berlin/Germany) within the cDNA sequencing consortium of the German
             Genome Project.
             No 81 sequence available.
             This clone (DKFp313N2433) is available at the RZPD in Berlin.
             Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
             Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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QY      61  CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 120
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DB      255 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 314
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QY      121 TGTCTCTTGTGATCTGTATCATCTGTCATCTCTGA 159
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DB      315 TGTCTCTTGTGATCTGTATCATCTGTCATCTCTCTGA 353
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RESULT 43
BP257291      560 bp mRNA linear EST 16-SEP-2004
LOCUS         BP257291 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION    HRT00595, mRNA sequence.
ACCESSION     BP257291
VERSION       BP257291.1 GI:52172521
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE     1 (bases 1 to 560)
AUTHORS       Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
             Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE       Sequence comparison of human and mouse genes reveals a homologous
             block structure in the promoter regions
JOURNAL      Genome Res. 14 (9), 1711-1718 (2004)
PUBMED      15342556
COMMENT     Contact: Yutaka Suzuki
             Department of Virology
             Institute of Medical Science, University of Tokyo
             4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
             Email: ysuzuki@ims.u-tokyo.ac.jp.

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Db 242 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGCTCATCTTAATA 301

Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 159

Db 302 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 340

RESULT 45

LOCUS BP257982

DEFINITION BP257982 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT02342, mRNA sequence.

VERSION BP257982

KEYWORDS BP257982.1 GI:52173212

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 159

Db 304 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 342

RESULT 46

LOCUS BP258939

DEFINITION BP258939 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT05022, mRNA sequence.

VERSION BP258939

KEYWORDS BP258939.1 GI:52174169

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
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Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 184 ATGGAGAAAGTCCATATCTACTCGCTCAGCTATGAAGAGCCTCAACCAATTGAATG 243

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Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 159

Db 304 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 342

RESULT 47

LOCUS BP257744

DEFINITION BP257744 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT01757, mRNA sequence.

VERSION BP257744

KEYWORDS BP257744.1 GI:52172974

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Db 256 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315

Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 159

Db 316 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 354

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Qy 61 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120

Db 256 CCTCAACAGCAGCTCAAAAGCTCAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315

Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 159

Db 316 TGTCTCTTCTGCTGATCTGATCATCATCGTGATGCTTCTCTGA 354

RESULT 47

LOCUS BP257744

DEFINITION BP257744 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT01757, mRNA sequence.

VERSION BP257744

KEYWORDS BP257744.1 GI:52172974

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTATCTTCTCTGA 159
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Db 283 TGTCTCTTGTGATCTGTATCATCGTATCGTATCTTCTCTGA 321
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RESULT 48
BP258507
LOCUS
DEFINITION BP258507 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT03670, mRNA sequence.
ACCESSION BP258507
VERSION BP258507.1 GI:52173737
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 562)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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LOCUS
DEFINITION BP257855 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT02035, mRNA sequence.
ACCESSION BP257855
VERSION BP257855.1 GI:52173085
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
1 (bases 1 to 563)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556

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Db 216 TGTCTCTTGTGATCTGTATCATCGTATCGTATCTTCTCTGA 254
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COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp

FEATURES

Location/Qualifiers
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